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3M protein - protein search, using sw model

run on: April 14, 2004, 15:40:43 ; Search time 22 Seconds
(without alignments)
1145.158 Million cell updates/sec

Title: US-09-632-722-2
Perfect score: 2634
Sequence: 1 MGRPLHLVLSASLAGLLLL.....RGLPKAKSHAPVITSSPLK 488

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptcdat2/iaa/5A-COMB.pep:*
2: /cgn2_6/ptcdat2/iaa/5B-COMB.pep:*
3: /cgn2_6/ptcdat2/iaa/6A-COMB.pep:*
4: /cgn2_6/ptcdat2/iaa/6B-COMB.pep:*
5: /cgn2_6/ptcdat2/iaa/PTUS-COMB.pep:*
6: /cgn2_6/ptcdat2/iaa/backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	2634	100.0	488	4	US-09-367-777-44 Sequence 47, Appl
2	2634	100.0	488	4	US-09-367-791A-27 Sequence 21, Appl
3	2557	97.1	488	1	US-08-487-037-1 Sequence 1, Appl
4	2441	92.7	448	5	PCT-US92-10068-1 Sequence 1, Appl
5	2439	92.6	448	1	US-08-295-411-3 Sequence 3, Appl
6	2439	92.6	448	2	US-08-955-471-3 Sequence 3, Appl
7	2439	92.6	448	5	PCT-US92-10242-3 Sequence 3, Appl
8	2249.5	85.4	437	1	US-08-487-037-2 Sequence 2, Appl
9	2241.5	85.1	437	1	US-08-487-037-3 Sequence 2, Appl
10	1851	70.3	482	1	US-08-469-486-2 Sequence 2, Appl
11	1851	70.3	482	2	US-08-469-486-2 Sequence 2, Appl
12	1847	70.1	487	1	US-08-469-486-53 Sequence 53, Appl
13	1847	70.1	487	2	US-08-469-486-53 Sequence 53, Appl
14	1631	61.9	306	1	US-08-330-978-1 Sequence 1, Appl
15	1631	61.9	306	1	US-08-474-042-1 Sequence 1, Appl
16	1631	61.9	306	1	US-08-484-558-1 Sequence 1, Appl
17	1631	61.9	306	1	US-08-774-592-1 Sequence 1, Appl
18	1354	51.4	254	1	US-08-330-978-3 Sequence 3, Appl
19	1354	51.4	254	1	US-08-474-042-3 Sequence 3, Appl
20	1354	51.4	254	1	US-08-484-558-3 Sequence 3, Appl
21	1354	51.4	254	1	US-08-774-592-3 Sequence 3, Appl
22	1305.5	49.6	247	3	US-08-944-483-49 Sequence 49, Appl
23	1289	48.9	241	1	US-08-330-978-4 Sequence 4, Appl
24	1289	48.9	241	1	US-08-474-042-4 Sequence 4, Appl
25	1289	48.9	241	1	US-08-484-558-4 Sequence 4, Appl
26	1289	48.9	241	1	US-08-774-592-4 Sequence 4, Appl
27	1051.5	39.9	461	6	5521070-2 Patent No. 5521070

28	1041.5	39.5	461	3	US-08-742-877-2 Sequence 2, Appl
29	1039.5	39.5	461	4	US-09-053-871A-21 Sequence 21, Appl
30	1039.5	39.5	461	4	US-10-133-907-5 Sequence 5, Appl
31	1002.5	38.1	415	1	US-08-073-531B-1 Sequence 1, Appl
32	1002.5	38.1	415	2	US-08-766-288-1 Sequence 1, Appl
33	996.5	37.8	415	4	US-09-118-748-2 Sequence 2, Appl
34	992.5	37.7	415	1	US-08-295-411-2 Sequence 2, Appl
35	992.5	37.7	415	2	US-08-955-471-2 Sequence 2, Appl
36	992.5	37.7	415	5	PCT-US92-10242-2 Sequence 2, Appl
37	952	36.1	444	1	US-08-475-845-2 Sequence 2, Appl
38	952	36.1	444	2	US-08-327-690-2 Sequence 2, Appl
39	952	36.1	444	2	US-08-660-289-2 Sequence 2, Appl
40	952	36.1	444	2	US-08-537-807-2 Sequence 2, Appl
41	952	36.1	444	2	US-08-871-003-2 Sequence 2, Appl
42	952	36.1	444	3	US-08-464-233-2 Sequence 2, Appl
43	952	36.1	444	3	US-09-189-607-2 Sequence 2, Appl
44	952	36.1	444	3	US-09-378-907-2 Sequence 2, Appl
45	952	36.1	444	5	PCT-US94-05779-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-367-777-44
Sequence 44, Application US/09367777
Patent No. 6562598
GENERAL INFORMATION:
APPLICANT: Himmelsbach, Michele
Pfleiderer, Michael
Falkner, Falko-Gunter
Eibl, Johann
Dorner, Friedrich
Schlokat, Uwe
TITLE OF INVENTION: Factor X Deletion Mutants and Analogues Thereof
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/367,777
FILING DATE: 10-NO. 6562598-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 336/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00046
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 20695D-0009000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 44;
US-09-367-777-44
Query Match 100.0%; Score 2634; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.5e-203;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRPLHLVLLSASLAGLLLGESLFRREQANNILARVTRANSFLEEMKKGHLRECEMEE 60
DB 1 MGRPLHLVLLSASLAGLLLGESLFRREQANNILARVTRANSFLEEMKKGHLRECEMEE 60
QY 61 TCSYEAREVFEEDSKTNEFWNKYKDGOCETSPCONQCKDGLGEYTCCTCLEGFEKN 120
DB 61 TCSYEAREVFEEDSKTNEFWNKYKDGOCETSPCONQCKDGLGEYTCCTCLEGFEKN 120
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DB 121 CELFTRKLCSLDNGDCDQFCHEEONSVCSCARGYTLADNGKACIPTGYPGCKOTLERR 180
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DB 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGNNLTRIVGQGE 240
QY 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEOEGGE 300
DB 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEOEGGE 300
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DB 301 AVHEVEVVIKHNRTKETDYDFDIAVLRLKPTITFRMNVAPACLPDRDWAESTLMTQKTI 360
QY 361 VSGFGRTHKGROSTRKMLLEVYVDNRNSCKLSSSFIITQNMFCAGYDTPKQDACAQGS 420
DB 361 VSGFGRTHKGROSTRKMLLEVYVDNRNSCKLSSSFIITQNMFCAGYDTPKQDACAQGS 420
QY 421 GPHVTRFKDITYFTVGIWSGESCARKGYGIYTKVTAFLKWIIDRSMTKRGLPKAKSHAPE 480
DB 421 GPHVTRFKDITYFTVGIWSGESCARKGYGIYTKVTAFLKWIIDRSMTKRGLPKAKSHAPE 480

RESULT 2
US-09-367-791A-27
; Sequence 27, Application US/09367791A
; Patent No. 6573071
; GENERAL INFORMATION:
; APPLICANT: Himmelsbach, Michele
; Schlokot, Uwe
; Dorrner, Friedrich
; Fisch, Andreas
; Eibl, Johann
; TITLE OF INVENTION: Factor X Analogues With
; a Modified Protease Cleavage Site
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/367.791A
; FILING DATE: 12-No. 6573071-1999
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-367-791A-27

Query Match 100.0%; Score 2634; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.5e-203;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRPLHLVLLSASLAGLLLGESLFRREQANNILARVTRANSFLEEMKKGHLRECEMEE 60
DB 1 MGRPLHLVLLSASLAGLLLGESLFRREQANNILARVTRANSFLEEMKKGHLRECEMEE 60
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DB 61 TCSYEAREVFEEDSKTNEFWNKYKDGOCETSPCONQCKDGLGEYTCCTCLEGFEKN 120
QY 121 CELFTRKLCSLDNGDCDQFCHEEONSVCSCARGYTLADNGKACIPTGYPGCKOTLERR 180
DB 121 CELFTRKLCSLDNGDCDQFCHEEONSVCSCARGYTLADNGKACIPTGYPGCKOTLERR 180
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGNNLTRIVGQGE 240
DB 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGNNLTRIVGQGE 240
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DB 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEOEGGE 300
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DB 301 AVHEVEVVIKHNRTKETDYDFDIAVLRLKPTITFRMNVAPACLPDRDWAESTLMTQKTI 360
QY 361 VSGFGRTHKGROSTRKMLLEVYVDNRNSCKLSSSFIITQNMFCAGYDTPKQDACAQGS 420
DB 361 VSGFGRTHKGROSTRKMLLEVYVDNRNSCKLSSSFIITQNMFCAGYDTPKQDACAQGS 420
QY 421 GPHVTRFKDITYFTVGIWSGESCARKGYGIYTKVTAFLKWIIDRSMTKRGLPKAKSHAPE 480
DB 421 GPHVTRFKDITYFTVGIWSGESCARKGYGIYTKVTAFLKWIIDRSMTKRGLPKAKSHAPE 480
QY 481 VITSSPLK 488
DB 481 VITSSPLK 488

RESULT 3
US-08-487-037-1
; Sequence 1, Application US/08487037
; Patent No. 5795863
; GENERAL INFORMATION:
; APPLICANT: Wolf, David L.
; TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/487,037
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
FEATURE:
NAME/KEY: Modified-site
LOCATION: -17
OTHER INFORMATION: /note= "Location of Intron A"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (37-38)
OTHER INFORMATION: /note= "Location of Intron B"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 46
OTHER INFORMATION: /note= "Location of Intron C"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 63
OTHER INFORMATION: /note= "Amino acid represented by the greek letter Beta"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 84
OTHER INFORMATION: /note= "Location of Intron D"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 128
OTHER INFORMATION: /note= "Location of Intron E"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (209-210)
OTHER INFORMATION: /note= "Location of Intron F"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 249
OTHER INFORMATION: /note= "Location of Intron G"
FEATURE:
NAME/KEY: Peptide
LOCATION: -40..0
OTHER INFORMATION: /note= "Pre-Pro leader sequence"
FEATURE:
NAME/KEY: Protein
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor Xa- Light chain"
FEATURE:
NAME/KEY: Peptide
LOCATION: 143..194

OTHER INFORMATION: /note= "Activation Peptide"
FEATURE:
NAME/KEY: Protein
LOCATION: 195..448
OTHER INFORMATION: /note= "Factor Xa-Heavy Chain"
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: Group(17..22, 50..61, 55..70, 72..81, 89..100, 96
LOCATION: ..109, 111..124, 132..302, 201..206, 221..237,
LOCATION: 350..364, 375..403)
US-08-487-037-1
Query Match 97.1%; Score 2557; DB 1; Length 488;
Best Local Similarity 97.3%; Pred. No. 5.3e-197;
Matches 475; Conservative 13; Indels 0; Gaps 0;
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DB 1 MGRPLHLVLSASLAGLLLGESLPIRREOANNILARVTRANSFLEEMKKGHLRECEEE 60
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DB 61 TCSYTTARTVFTDSKTNFNNKYKDGQCEPSCQNGKCKXGLGEYTCCTCLEGEGKN 120
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DB 121 CELFTKCLSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKOTLERR 180
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DB 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEEGEGE 300
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DB 301 AVHEVEVWIKHNRFTKETDYDFDIIVLRKLTPIITPRMNVAPACLPDRDWAESTLMTQKTI 360
QY 361 VSGFGRTHEKGRQSTRKLMLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 420
DB 361 VSGFGRTHEKGRQSTRKLMLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 420
QY 421 GPHVTRFKDTYFTVGIVSMGESCARKGYIKYTKTAFLEKWDIDRSMKTRGLPKAKSHAPE 480
DB 421 GPHVTRFKDTYFTVGIVSMGESCARKGYIKYTKTAFLEKWDIDRSMKTRGLPKAKSHAPE 480
QY 481 VITSSPLK 488
DB 481 VITSSPLK 488

RESULT 4
PCT-US92-10068-1
Sequence 1, Application PC/TUS9210068
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C
APPLICANT: Edgington, Thomas S
APPLICANT: Fair, Daryl S
TITLE OF INVENTION: Factor X-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Inflammation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:

461 WIDRSMKTRGLPKAKSHAPEVITSSPLK 488
421 WIDRSMKTRGLPKAKSHAPEVITSSPLK 448

QY DB

RESULT 5
US-08-295-411-3
; Sequence 3, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: For Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1-139
; OTHER INFORMATION: /note= "Factor X Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 140-142
; OTHER INFORMATION: /note= "Factor X Connecting
; OTHER INFORMATION: Tripeptide"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 143-448
; OTHER INFORMATION: /note= "Factor X Heavy Chain"
US-08-295-411-3
Query Match 92.6%; Score 2439; DB 1; Length 448;
Best Local Similarity 99.6%; Pred. No. 1.4e-187;
Matches 446; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 ANSFLEMKKGLHRECEMEETCSYEAREVEFSDSKNEFWNKYKDGQDCQETSPCONQK 100

Db 1 ANSFLEEMKKGHLERECWECTSYEAREVFEDSDKTNEFWNKYKDGOCETSPQCNQK 60
Qy 101 CKDGLGEYTCCTLEGFEGKNCLEFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADN 160
Db 61 CKBGLGEYTCCTLEGFEGKNCLEFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADN 120
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Db 121 GKACIPGPGCGQTILERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDF 180
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Db 181 NOTQPERGDNLTIRIVGQCKGECPCWQALLINEENEGFCGGTILSEFYILTAHCLYQ 240
Qy 281 AKRFKRVGDRNTEQEGGGAHVVEVVIKHNFTKETYDFDIKLVRLKTPITFRMNVAP 340
Db 241 AKRFKRVGDRNTEQEGGGAHVVEVVIKHNFTKETYDFDIKLVRLKTPITFRMNVAP 300
Qy 341 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQ 400
Db 301 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQ 360
Qy 401 NMFCAGYDTKQEDACQDGGPHVTRFKDTYFVTGIVSWGESCARKGKIYTKVTAFLK 460
Db 361 NMFCAGYDTKQEDACQDGGPHVTRFKDTYFVTGIVSWGESCARKGKIYTKVTAFLK 420
Qy 461 WIDRSMKTRGLPKAKSHAPEVITSSPLK 488
Db 421 WIDRSMKTRGLPKAKSHAPEVITSSPLK 448

RESULT 6
US-08-955-471-3
; Sequence 3, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968/51th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSPR263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..139
; OTHER INFORMATION: /note= "Factor X Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 140..142
; OTHER INFORMATION: /note= "Factor X Connecting
; OTHER INFORMATION: Tripeptide"
; NAME/KEY: Region
; LOCATION: 143..448
; OTHER INFORMATION: /note= "Factor X Heavy Chain"
; US-08-955-471-3
Query Match 92.6%; Score 2439; DB 2; Length 448;
Best Local Similarity 99.6%; Pred. No. 1.4e-187;
Matches 448; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 41 ANSFLEEMKKGHLERECWECTSYEAREVFEDSDKTNEFWNKYKDGOCETSPQCNQK 100
Db 1 ANSFLEEMKKGHLERECWECTSYEAREVFEDSDKTNEFWNKYKDGOCETSPQCNQK 60
Qy 101 CKDGLGEYTCCTLEGFEGKNCLEFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADN 160
Db 61 CKBGLGEYTCCTLEGFEGKNCLEFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADN 120
Qy 161 GKACIPGPGCGQTILERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDF 220
Db 121 GKACIPGPGCGQTILERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDF 180
Qy 221 NOTQPERGDNLTIRIVGQCKGECPCWQALLINEENEGFCGGTILSEFYILTAHCLYQ 280
Db 181 NOTQPERGDNLTIRIVGQCKGECPCWQALLINEENEGFCGGTILSEFYILTAHCLYQ 240
Qy 281 AKRFKRVGDRNTEQEGGGAHVVEVVIKHNFTKETYDFDIKLVRLKTPITFRMNVAP 340
Db 241 AKRFKRVGDRNTEQEGGGAHVVEVVIKHNFTKETYDFDIKLVRLKTPITFRMNVAP 300
Qy 341 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQ 400
Db 301 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQ 360
Qy 401 NMFCAGYDTKQEDACQDGGPHVTRFKDTYFVTGIVSWGESCARKGKIYTKVTAFLK 460
Db 361 NMFCAGYDTKQEDACQDGGPHVTRFKDTYFVTGIVSWGESCARKGKIYTKVTAFLK 420
Qy 461 WIDRSMKTRGLPKAKSHAPEVITSSPLK 488
Db 421 WIDRSMKTRGLPKAKSHAPEVITSSPLK 448

RESULT 7
PCT-US92-10242-3
; Sequence 3, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA

COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLSCULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor X Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting
OTHER INFORMATION: Tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
PCT-US92-10242-3
Query Match 92.6%; Score 2439; DB 5; Length 448;
Best Local Similarity 99.6%; Pred. No. 1.4e-187;
Matches 446; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 41 ANSFLKMKHLEKRECEMEETCSYEAREVEFSDKTNFANKYKGDQDQCTSPQONQK 100
DB 1 ANSFLKMKHLEKRECEMEETCSYEAREVEFSDKTNFANKYKGDQDQCTSPQONQK 60
QY 101 CKDGLGYTCTCLEGFEKNCLELTKRLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADN 160
DB 61 CKBGLGYTCTCLEGFEKNCLELTKRLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADN 120
QY 161 GKACIPGPGKQTLERRKRSVAQTSSGEAPDSITWKPYDAADLDPTENPFDLLDF 220
DB 121 GKACIPGPGKQTLERRKRSVAQTSSGEAPDSITWKPYDAADLDPTENPFDLLDF 180
QY 221 NOTQPERGDNLTIRVGGCEKDCGCPQALLINEEGFCGGTILSERVILTAACHLQ 280
DB 181 NOTQPERGDNLTIRVGGCEKDCGCPQALLINEEGFCGGTILSERVILTAACHLQ 240
QY 281 AKRFKRVGDRNTEQEGEAVHEVVIKHNRTKETDYFDIAVLRLKTPITFRMNVAP 340
DB 241 AKRFKRVGDRNTEQEGEAVHEVVIKHNRTKETDYFDIAVLRLKTPITFRMNVAP 300
QY 341 ACLPBRDAESTMTQKTGIVSGRTHKGRQSTRKLMLEVPVDRNSCKLSSSIITQ 400
DB 301 ACLPBRDAESTMTQKTGIVSGRTHKGRQSTRKLMLEVPVDRNSCKLSSSIITQ 360
QY 401 NMFCAGYDTKQEDACQDGSQGPVHTFKDTYFVTGIVSWGECARKGKIYTKVTAFLK 460

Db 361 NMFCAGYDTKQEDACQDGSQGPVHTFKDTYFVTGIVSWGECARKGKIYTKVTAFLK 420
QY 461 WIDRSMKTRGLPKAKSHAPVITSSPLK 488
Db 421 WIDRSMKTRGLPKAKSHAPVITSSPLK 448
RESULT 8
US-08-487-037-2
Sequence 2, Application US/08487037
Patent No. 5795863
GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
FEATURE:
NAME/KEY: Protein
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor Xa-Light Chain"
FEATURE:
NAME/KEY: Peptide
LOCATION: -40..0
OTHER INFORMATION: /note= "Pre-Pro leader sequence"
FEATURE:
NAME/KEY: Modified-site
LOCATION: -17
OTHER INFORMATION: /note= "Location of Intron A"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (37^38)
OTHER INFORMATION: /note= "Location of Intron B"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 46
OTHER INFORMATION: /note= "Location of Intron C"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 63
OTHER INFORMATION: /note= "An amino acid represented
OTHER INFORMATION: by the greek letter Beta"
FEATURE:
NAME/KEY: Modified-site

LOCATION: 84
OTHER INFORMATION: /note= "Location of Intron D"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 128
OTHER INFORMATION: /note= "Location of Intron E"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (158*159)
OTHER INFORMATION: /note= "Location of Intron F"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 198
OTHER INFORMATION: /note= "Location of Intron G"
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: Group(17..22, 50..61, 55..70, 72..81, 89..100, 96
LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
LOCATION: 299..313, 324..352)
IS-08-487-037-2

Query Match 85.4%; Score 2249.5; DB 1; Length 437;
Best Local Similarity 86.9%; Pred. No. 28-172;
Matches 424; Conservative 0; Mismatches 13; Indels 51; Gaps 1;

1 MGRPLHLVLLSASLAGLLGSLRIRREQANNILARVTRANSFLEEMKKGHLRECEWEE 60
1 MGRPLHLVLLSASLAGLLGSLRIRREQANNILARVTRANSFLEEMKKGHLRTRTMTT 60
61 TCSYEAEARVFDSDKTNFNNKYKDGOCETSPQONOGKCKDGLGYETCTCLGFEFGKN 120
61 TCSYTTARTVFDSDKTNFNNKYKDGOCETSPQONOGKCKXGLGYETCTCLGFEFGKN 120
121 CELFTRKCLSLDNGDCDFCHEEONSVCARGYTLADNGKACIPGYPGCKQTLLRR 180
121 CELFTRKCLSLDNGDCDFCHEEONSVCARGYTLADNGKACIPGYPGCKQTLLRR 180
181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPDLDFNQTOPFERGDNMLTIVGGQE 240
181 KR-----RIVGGQE 189
241 CXDGCPQWALLINENEGFCGGTILSBFYILTAACHLYQAKRFKVRVGRNTEQESGGE 300
190 CXDGCPQWALLINENEGFCGGTILSBFYILTAACHLYQAKRFKVRVGRNTEQESGGE 249
301 AVHEVEVWKHNRFTKTYDPIAVLRKLTPTTFMNVAPACLPERDWAESTLMTQKTI 360
250 AVHEVEVWKHNRFTKTYDPIAVLRKLTPTTFMNVAPACLPERDWAESTLMTQKTI 309
361 VSGFGTHKGRQSTELKMLEVYVDRNSCKLSSFIITQNMFCAGYDTQEDACQDSDG 420
310 VSGFGTHKGRQSTELKMLEVYVDRNSCKLSSFIITQNMFCAGYDTQEDACQDSDG 369
421 GPHVTRFKDTYFTVTGIVSWGESCARKGYGYTKVTAFLKWDIDRSMKTRGLPRAKSHAPE 480
370 GPHVTRFKDTYFTVTGIVSWGESCARKGYGYTKVTAFLKWDIDRSMKTRGLPRAKSHAPE 429
481 VITSSPLK 488
430 VITSSPLK 437

RESULT 9
S-08-487-037-3
Sequence 3. Application US/08487037
Patent No. 5795863
GENERAL INFORMATION:
APPLICANT: Welf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
FEATURE:
NAME/KEY: Modified-site
LOCATION: -40..397
OTHER INFORMATION: /note= "Same features apply from
OTHER INFORMATION: SEQ ID NO:2"
FEATURE:
NAME/KEY: Protein
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor Xa - Light Chain"
FEATURE:
NAME/KEY: Peptide
LOCATION: -40..0
OTHER INFORMATION: /note= "Pre-Pro leader sequence"
FEATURE:
NAME/KEY: Modified-site
LOCATION: -17
OTHER INFORMATION: /note= "Location of Intron A"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (37*38)
OTHER INFORMATION: /note= "Location of Intron B"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 46
OTHER INFORMATION: /note= "Location of Intron C"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 63
OTHER INFORMATION: /note= "An amino acid represented
OTHER INFORMATION: by the greek letter Beta"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 84
OTHER INFORMATION: /note= "Location of Intron D"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (158*159)
OTHER INFORMATION: /note= "Location of Intron F"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 198
OTHER INFORMATION: /note= "Location of Intron G"
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: Group(17..22, 50..61, 55..70, 72..81, 89..100, 96
LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,

LOCATION: 299..313, 324..352)
US-08-469-037-3

Query Match 85.1%; Score 2241.5; DB 1; Length 437;
Best Local Similarity 86.5%; Pred. No. 8.9e-172;
Matches 422; Conservative 2; Mismatches 13; Indels 51; Gaps 1;

QY 1 MGRPLHLVLSASLAGLLIGESLFRIRBOANNILARVTRANSFLRRECMHRECMEE 60
DB 1 MGRPLHLVLSASLAGLLIGESLFRIRBOANNILARVTRANSFLRRECMHRECMEE 60
QY 61 TCSVEEAREVFEDSDKNEFWNKYKDDOCETSPCONQCKKDGLEYTCTCLEFEGKN 120
DB 61 TCSVTTARTVFTSDKNTFNWYKDDOCETSPCONQCKKDGLEYTCTCLEFEGKN 120
QY 121 CELFTRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGYPGKOTLERR 180
DB 121 CELFTRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGYPGKOTLERR 180
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTEPNPDLDFNQTPERGNNLTRIVGGQE 240
DB 181 KR-----RIVGGQE 189
QY 241 CKGECFPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEGGE 300
DB 190 CKGECFPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEGGE 249
QY 301 AVHEVEVVIKINRTKTYDFDIAVLRLKTPITFRMNVAPACLPEDWAEISTMTQKTI 360
DB 250 AVHEVEVVIKINRTKTYDFDIAVLRLKTPITFRMNVAPACLPEDWAEISTMTQKTI 309
QY 361 VSGFGRTHKGRQSTRLMLEVPYVDRNSCKLSSFFITQNMPCAGYDTKQEDACQDGG 420
DB 310 VSGFGRTHKGRQSTRLMLEVPYVDRNSCKLSSFFITQNMPCAGYDTKQEDACQDGG 369
QY 421 GPHVTRKDTYFVTGIVSWGEGCARKGKGYITKVTAFKWDIDRSMKTRGLPKAKSH 480
DB 370 GPHVTRKDTYFVTGIVSWGEGCARKGKGYITKVTAFKWDIDRSMKTRGLPKAKSH 429
QY 481 VITSSPLK 488
DB 430 VITSSPLK 437

RESULT 10
US-08-469-486-2
; Sequence 2, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thøgersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: Improved proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-2
Query Match 70.3%; Score 1851; DB 1; Length 492;
Best Local Similarity 69.8%; Pred. No. 2.1e-140;
Matches 340; Conservative 58; Mismatches 81; Indels 8; Gaps 4;
QY 5 LHLVLASLAGLLIGESLFRIRBOANNILARVTRANSFLRRECMHRECMEE 64
DB 5 LHLVLSTALGILLRPAQSVFLPRQAHRLVLRQARRANSFLRRECMHRECMEE 64
QY 65 EEARVFEEDSDKNEFWNKYKDDOCETSPCONQCKKDGLEYTCTCLEFEGKN 124
DB 65 EEARVFEEDSDKNEFWNKYKDDOCETSPCONQCKKDGLEYTCTCLEFEGKN 124
QY 125 TRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGYPGKOTLERR 184
DB 125 TRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGYPGKOTLERR 182
QY 185 AQATSSSGEAPDSITWKPYDAADLDPTEPNPDLDFNQTPERGNNLTRIVGGQE 242
DB 183 -WAHTESEALDASELHYDPAQLSPTESLGLGINTETPSAGDGSQVVRIVGRDCA 241
QY 243 DGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEGGE 302
DB 242 DGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEGGE 301
QY 303 HEVEVVIKINRTKTYDFDIAVLRLKTPITFRMNVAPACLPEDWAEISTMTQKTI 362
DB 302 HEVEVVIKINRTKTYDFDIAVLRLKTPITFRMNVAPACLPEDWAEISTMTQKTI 361
QY 363 GFGRTHEKGRQSTRLMLEVPYVDRNSCKLSSFFITQNMPCAGYDTKQEDACQDGG 422
DB 362 GFGRTHEKGRQSTRLMLEVPYVDRNSCKLSSFFITQNMPCAGYDTKQEDACQDGG 421
QY 423 HVTRFKDTYFVTGIVSWGEGCARKGKGYITKVTAFKWDIDRSMKTRGLPKAKSH 479
DB 422 HVTRFKDTYFVTGIVSWGEGCARKGKGYITKVTAFKWDIDRSMKTRGLPKAKSH 479
QY 480 EVITSSP 486
DB 482 ATWVTP 488
RESULT 11
US-08-469-658-2
; Sequence 2, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Thøgersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-658-2

Query Match 70.3%; Score 1851; DB 2; Length 492;

Best Local Similarity 69.8%; Pred. No. 2.1e-140;

Matches 340; Conservative 58; Mismatches 81; Indels 8; Gaps 4;

QY 5 LHLVLLSASLAGLLGSLFIRREQANNILARVTRANSFLERMKKGLHRECMETCSY 64
DB 5 LHLVLLSALGALLRPAAGSVFLPRDQARVLRQARRANSFLERVKQGNLERECLEACSL 64
QY 65 BEAREVFEDSDKTNEFWNKYKDGQCEPSCQNGKCKDGLGEYTCCTCLEGEGKNCLEF 124
DB 65 BEAREVFEDAEQTDPEFWSKYKDGQCEGHCPLNQGHCKDGIQDYTCCTCAEGEGKNCERFS 124
QY 125 TRKLCSDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERKRSV 184
DB 125 TREICSLDNGGCDQFCHEERSEVRCSAHGYVLGDDSKSCVSTERFPCKFTQGRSRR-- 182
QY 185 AQATSSSGEAPDSITWKPYDAADLDPTENPDLDFNQTQPERGD--NNLTRIVGQECK 242
DB 183 -WAHTSEDALDASELEHYDPADLSPTESSLDLLGLNRTPEPSAGEDSGSVRIVGRDCA 241
QY 243 DGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDNTQEGEGRAV 302
DB 242 EGCECPWQALLVNEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDNTQEGEGRAV 301
QY 303 HEVEMTKHNRFTKTYDFOIAVLRLKTPITFRNVPAPACLPEDWABSTLMTQKTGIVS 362
DB 302 HEVEMTKHNSFVKZETDFOIAVLRLKTPITFRNVPAPACLPEDWABSTLMTQKTGIVS 361
QY 363 GFGTHKRGQSTLKLMLVPPYDRNSCKLSSSFTITQNMFCAGYDTKQEDACQDSGAP 422
DB 362 GFGTHKRGKSLSTLKLMLVPPYDRNSCKLSSSFTITQNMFCAGYDTKQEDACQDSGAP 421
QY 423 HVTRFKDTYFVTGIVSVSGECARGKGYITKYATLKWIDRSMKTR-GLPKAKSH--AP 479
DB 422 HVTRFKDTYFVTGIVSVSGECARGKRGFVTKVSNFLKWIDKIMKARAGARGHSEAP 481
QY 480 EVITSSP 486

DB 482 ATWTVPP 488

RESULT 12

US-08-469-486-53
Sequence 53, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Thøgersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
NUMBER OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-53

Query Match 70.1%; Score 1847; DB 1; Length 487;

Best Local Similarity 70.4%; Pred. No. 4.3e-140;

Matches 336; Conservative 59; Mismatches 76; Indels 6; Gaps 3;

QY 5 LHLVLLSASLAGLLGSLFIRREQANNILARVTRANSFLERMKKGLHRECMETCSY 64
DB 5 LHLVLLSALGALLRPAAGSVFLPRDQARVLRQARRANSFLERVKQGNLERECLEACSL 64
QY 65 BEAREVFEDSDKTNEFWNKYKDGQCEPSCQNGKCKDGLGEYTCCTCLEGEGKNCLEF 124
DB 65 BEAREVFEDAEQTDPEFWSKYKDGQCEGHCPLNQGHCKDGIQDYTCCTCAEGEGKNCERFS 124
QY 125 TRKLCSDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERKRSV 184
DB 125 TREICSLDNGGCDQFCHEERSEVRCSAHGYVLGDDSKSCVSTERFPCKFTQGRSRR-- 182
QY 185 AQATSSSGEAPDSITWKPYDAADLDPTENPDLDFNQTQPERGD--NNLTRIVGQECK 242
DB 183 -WAHTSEDALDASELEHYDPADLSPTESSLDLLGLNRTPEPSAGEDSGSVRIVGRDCA 241
QY 243 DGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDNTQEGEGRAV 302

Db 242 EGCEPWALLVNEENEGCGGTTILNEFYVLTAAHCLHQAARFTVRVGDNRNTEQEGNEWA 301
QY 303 HEVEVVIKHNFTKETYDFDIIVLRLKTPITFRMVNAPACLPERDWAESTLMTQKTGIYS 362
Db 302 HEVEMTVKHSRFTKETYDFDIIVLRLKTPITFRMVNAPACLPERDWAESTLMTQKTGIYS 361
QY 363 GFRGTHKGRSTRKMLKLEVPYVDRNSCKLSSSFTITONMFCAGYDTKOEDACQDGGP 422
Db 362 GFRGTHKGRSTRKMLKLEVPYVDRNSCKLSSSFTITONMFCAGYDTKOEDACQDGGP 421
QY 423 HVTRFKDTYFTVTGIVSWGESCARKGKGIYTKVTAFLKWDIRSMKTR-GLPKAKSHA 478
Db 422 HVTRFKDTYFTVTGIVSWGESCARKGKGIYTKVTAFLKWDIRSMKTR-GLPKAKSHA 478

RESULT 13

US-08-469-658-53
; Sequence 53, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egeresen, Hans Christian
; APPLICANT: Holter, Thor Las
; APPLICANT: Ezerodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
; PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-658-53

Query Match 70.1%; Score 1847; DB 2; Length 487;
Best Local Similarity 70.4%; Pred. No. 4.38-140;
Matches 336; Conservative 59; Mismatches 76; Indels 6; Gaps 3;
QY 5 LHLVLLSASLGLLLGSLFIRREQANILARVTRANSFLEEMKXGHLERECMEETCSY 64
Db 5 LHLVLLSALGGLLRPGAGSVFLPRDQAHVLRQARRANSFLEEVKQGNLERECLEBACSL 64

QY 65 EBAREVEDSKTNEFWNYKDGDCQETSPCQNGKCKDGLCEYTCCTCLEGEGKNCCLF 124
Db 65 EBAREVEDAEQDDEFWSKYDGDQCEGHPCLNQGHCKDGIQDYTCCTCAEGEGKNCSEFS 124
QY 125 TRKLCSDNDCQDFCHEEQNSVVCSCARGYTLADNGKACIPTGPVPCGKQTLERRKRSV 184
Db 125 TREICSLDNGCQDFCREERSEVRGSCAHGYVLGDDSKSCVSTERFFCGKFTQGRSRR-- 182
QY 185 ACATSSSGEAPDITWKPYPDAADLDTEPFLLDFNCTQPERGD--NNLTIRIVGGQECK 242
Db 183 -WAIHTSEDALDASELHYDPADLSPTESSLDLLGNRTPEPSAGEDSGSVRIVGGRDCA 241
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Db 242 EGCEPWQALLVNEENEGCGGTTILNEFYVLTAAHCLHQAARFTVRVGDNRNTEQEGNEWA 301
QY 303 HEVEVVIKHNFTKETYDFDIIVLRLKTPITFRMVNAPACLPERDWAESTLMTQKTGIYS 362
Db 302 HEVEMTVKHSRFTKETYDFDIIVLRLKTPITFRMVNAPACLPERDWAESTLMTQKTGIYS 361
QY 363 GFRGTHKGRSTRKMLKLEVPYVDRNSCKLSSSFTITONMFCAGYDTKOEDACQDGGP 422
Db 362 GFRGTHKGRSTRKMLKLEVPYVDRNSCKLSSSFTITONMFCAGYDTKOEDACQDGGP 421
QY 423 HVTRFKDTYFTVTGIVSWGESCARKGKGIYTKVTAFLKWDIRSMKTR-GLPKAKSHA 478
Db 422 HVTRFKDTYFTVTGIVSWGESCARKGKGIYTKVTAFLKWDIRSMKTR-GLPKAKSHA 478

RESULT 14

US-08-330-978-1
; Sequence 1, Application US/08330978
; Patent No. 5589571
; GENERAL INFORMATION:
; APPLICANT: King, Robert
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
; TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,978
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,558
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Muraehige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0007.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)887-1500
; TELEFAX: (202)822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond

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; LOCATION: 59...64
; FEATURE: Disulfide-bond
; NAME/KEY: Disulfide-bond
; LOCATION: 79...95
; FEATURE: Disulfide-bond
; NAME/KEY: Disulfide-bond
; LOCATION: 160
; OTHER INFORMATION: /note= "Disulfide linkage to
; OTHER INFORMATION: residue 132 of SEQ ID NO:2"
; FEATURE: Disulfide-bond
; NAME/KEY: Disulfide-bond
; LOCATION: 208...222
; FEATURE: Disulfide-bond
; NAME/KEY: Disulfide-bond
; LOCATION: 233...261
; LOCATION: 233...261
US-08-330-978-1

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Best Local Similarity 99.7%; Pred. No. 4.9e-123;
Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 SVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNCTQPERGDNLTTRIVGGQECK 60

QY 243 DGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVYVDRNTEQEGGEAV 302
Db 61 DGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVYVDRNTEQEGGEAV 120

QY 303 HEVEVVIKHNRFKETYDFDIIVLRKLTPTTFMNVAPACLPDRDWAESTLMTQKTGIVS 362
Db 121 HEVEVVIKHNRFKETYDFDIIVLRKLTPTTFMNVAPACLPDRDWAESTLMTQKTGIVS 180

QY 363 GFGRTHKGROSTRKLMLEVYVYVDRNSCKLSSSFIIITQNMFCAGYDTKQEDACQDSDGGP 422
Db 181 GFGRTHKGROSTRKLMLEVYVYVDRNSCKLSSSFIIITQNMFCAGYDTKQEDACQDSDGGP 240

QY 423 HVTRFKDTYFTVTGIVSWGESCARKGKGYITKVTAFKWDIDRSMKTRGLPKAKSHAPEVI 482
Db 241 HVTRFKDTYFTVTGIVSWGESCARKGKGYITKVTAFKWDIDRSMKTRGLPKAKSHAPEVI 300

QY 483 TSSPLK 488
Db 301 TSSPLK 306
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RESULT 15

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US-08-474-042-1
; Sequence 1, Application US/08474042
; Patent No. 5589572
; GENERAL INFORMATION:
; APPLICANT: King, Robert
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
; TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,042
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,558
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; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0007.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)887-1500
; TELEFAX: (202)822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 59...64
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 79...95
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 160
; OTHER INFORMATION: /note= "Disulfide linkage to
; OTHER INFORMATION: residue 132 of SEQ ID NO:2"
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 208...222
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 233...261
; LOCATION: 233...261
US-08-474-042-1

Query Match 61.9%; Score 1631; DB 1; Length 306;
Best Local Similarity 99.7%; Pred. No. 4.9e-123;
Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 SVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNCTQPERGDNLTTRIVGGQECK 242
Db 1 SVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNCTQPERGDNLTTRIVGGQECK 60

QY 243 DGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVYVDRNTEQEGGEAV 302
Db 61 DGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVYVDRNTEQEGGEAV 120

QY 303 HEVEVVIKHNRFKETYDFDIIVLRKLTPTTFMNVAPACLPDRDWAESTLMTQKTGIVS 362
Db 121 HEVEVVIKHNRFKETYDFDIIVLRKLTPTTFMNVAPACLPDRDWAESTLMTQKTGIVS 180

QY 363 GFGRTHKGROSTRKLMLEVYVYVDRNSCKLSSSFIIITQNMFCAGYDTKQEDACQDSDGGP 422
Db 181 GFGRTHKGROSTRKLMLEVYVYVDRNSCKLSSSFIIITQNMFCAGYDTKQEDACQDSDGGP 240

QY 423 HVTRFKDTYFTVTGIVSWGESCARKGKGYITKVTAFKWDIDRSMKTRGLPKAKSHAPEVI 482
Db 241 HVTRFKDTYFTVTGIVSWGESCARKGKGYITKVTAFKWDIDRSMKTRGLPKAKSHAPEVI 300

QY 483 TSSPLK 488
Db 301 TSSPLK 306
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Search completed: April 14, 2004, 15:41:22
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 14, 2004, 15:40:44 ; Search time 47 Seconds
(without alignments)
2753.708 Million cell updates/sec

Title: US-09-632-722-2
Perfect score: 2634
Sequence: 1 MGRPLHLVLSASLAGLLLL.....RGLPKAKSHAPEVITSSPLK 488

Scoring table: BLOSUM62
Gapex 10.0, Gapext 0.5

Searched: 1082010 seqs, 265213723 residues

Total number of hits satisfying chosen parameters: 1082010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2634	100.0	488	14	US-10-407-123-27
3	2630	99.8	488	12	US-10-406-031-27
4	1646	62.5	309	15	US-10-360-101-233
5	1251	47.5	467	12	US-10-406-031-5
6	1238	47.0	467	12	US-10-406-031-2
7	1238	47.0	467	12	US-10-406-031-8
8	1223	46.4	455	12	US-10-406-031-17
9	1222	46.4	454	12	US-10-406-031-11
10	1216	46.2	453	12	US-10-406-031-14
11	1135.5	43.1	376	12	US-10-406-031-31
12	1041.5	39.5	461	9	US-09-894-901-3
13	1041.5	39.5	461	14	US-10-234-406-8
14	1041.5	39.5	461	16	US-10-038-854-92
15	1041.5	39.5	461	16	US-10-239-498A-5

16	1039.5	39.5	456	16	US-10-038-854-95
17	1039.5	39.5	456	16	US-10-038-854-96
18	1039.5	39.5	461	14	US-10-132-829-5
19	1039.5	39.5	461	14	US-10-234-406-6
20	1039.5	39.5	461	14	US-10-133-907-5
21	1039.5	39.5	461	16	US-10-038-854-93
22	1038.5	39.4	461	16	US-10-038-854-94
23	1032	39.2	462	12	US-10-411-037-10
24	1032	39.2	462	12	US-10-411-037-10
25	1026	39.0	456	12	US-10-406-031-28
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30	953	36.2	444	12	US-10-411-026-8
31	948	36.0	466	14	US-10-017-122-2
32	948	36.0	466	15	US-10-375-741-14
33	909.5	34.5	406	10	US-09-782-587B-3
34	909.5	34.5	406	15	US-10-383-898-1
35	905.5	34.4	405	16	US-10-360-101-225
36	865	32.8	394	16	US-10-038-854-6
37	852.5	32.4	406	10	US-09-782-587B-1
38	852.5	32.4	406	14	US-10-109-498-1
39	852.5	32.4	406	14	US-10-255-032-1
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41	852.5	32.4	406	15	US-10-386-898-7
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43	827	31.4	461	10	US-09-978-917A-2
44	827	31.4	461	12	US-09-997-623-2
45	827	31.4	461	14	US-10-182-263-2

ALIGNMENTS

RESULT 1

US-10-348-504-44
Sequence 44, Application US/10348504
Publication No. US20030138914A1
GENERAL INFORMATION:
APPLICANT: Himmelspach, Michele
Pfleiderer, Michael
Falkner, Falko-Gunter
Eibl, Johann
Dorner, Friedrich
Schlokat, Uwe
TITLE OF INVENTION: Factor X Deletion Mutants and Analogues Thereof
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/348,504
FILING DATE: 29-Jan-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/367,777
FILING DATE: 10-No. US20030138914A1-1999
APPLICATION NUMBER: AT A 336/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00046
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:

Sequence 95, Appl
Sequence 96, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 5, Appl
Sequence 93, Appl
Sequence 94, Appl
Sequence 10, Appl
Sequence 10, Appl
GENERAL INFORMATI
Sequence 2, Appl
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Sequence 8, Appl
Sequence 34, Appl
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Sequence 25, App
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Sequence 1, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 36, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl

NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 20695D-000900US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-348-504-44

Query Match 100.0%; Score 2634; DB 14; Length 488;
Best Local Similarity 100.0%; Pred. No. 8e-211;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 121 CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPGYPCKGQTLERR 180
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DB 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGGE 300
QY 301 AVHEVEVVIKHNRTKETYPDIAVLRKTPITFRMNVAPACLPERDWAESTLMTQKGTGI 360
DB 301 AVHEVEVVIKHNRTKETYPDIAVLRKTPITFRMNVAPACLPERDWAESTLMTQKGTGI 360
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DB 361 VSGFGRTHKGRQSTRKMLKLEVPYVDRNSCKLSSFFIITQNMFCAGYDTKQEDACQDGS 420
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DB 421 GPHVTRFKDTYFVTGIVSWGESCARKKGYGYTKVTAFLKWDIDRSMKTRGLPKAKSHAPE 480
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DB 481 VITSSPLK 488

RESULT 2
US-10-407-123-27
Sequence 27, Application US/10407123
Publication No. US20030181361A1
GENERAL INFORMATION:
APPLICANT: Himmelspach, Michele
Schlokat, Uwe
Dorner, Friedrich
Fisch, Andreas
Eibl, Johann
TITLE OF INVENTION: Factor X Analogues with
a Modified Protease Cleavage Site
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: PastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,123
FILING DATE: 04-Apr-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No. US20030181381A1-1999
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/80045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-407-123-27

Query Match 100.0%; Score 2634; DB 14; Length 488;
Best Local Similarity 100.0%; Pred. No. 8e-211;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGRPLHLVLLSASLAGLLLGESLFIREEQANNILARVTRANSFLEEMKKGHLERECMEE 60
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DB 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTOPERGDNNLTRIVGGQE 240
QY 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGGE 300
DB 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGGE 300
QY 301 AVHEVEVVIKHNRTKETYPDIAVLRKTPITFRMNVAPACLPERDWAESTLMTQKGTGI 360
DB 301 AVHEVEVVIKHNRTKETYPDIAVLRKTPITFRMNVAPACLPERDWAESTLMTQKGTGI 360
QY 361 VSGFGRTHKGRQSTRKMLKLEVPYVDRNSCKLSSFFIITQNMFCAGYDTKQEDACQDGS 420
DB 361 VSGFGRTHKGRQSTRKMLKLEVPYVDRNSCKLSSFFIITQNMFCAGYDTKQEDACQDGS 420
QY 421 GPHVTRFKDTYFVTGIVSWGESCARKKGYGYTKVTAFLKWDIDRSMKTRGLPKAKSHAPE 480
DB 421 GPHVTRFKDTYFVTGIVSWGESCARKKGYGYTKVTAFLKWDIDRSMKTRGLPKAKSHAPE 480

Db 421 GPHVTRFKDITVFTGIVSWGSCARKGKGIYTKVTAFLKWIIDRSMTKTRGLPKAKSHAP 480
QY 481 VITSSPLK 488
Db 481 VITSSPLK 488

RESULT 3
US-10-406-031-27
; Sequence 27, Application US/10406031
; Publication No. US20040043017A1
; GENERAL INFORMATION:
; APPLICANT: Masci, Paul Pantaleone
; APPLICANT: Lavin, Martin
; TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
; FILE REFERENCE: 15685-002001
; CURRENT APPLICATION NUMBER: US/10/406,031
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: AU 2003901033
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: AU PSI483
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-031-27

Query Match 99.8%; Score 2630; DB 12; Length 488;
Best Local Similarity 99.8%; Pred. No. 1.7e-210;
Matches 487; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGRPLHLVLLSASLAGLLLGESLFIREEQANILARVTPANSFLEEMKXHLRECMEE 60
Db 1 MGRPLHLVLLSASLAGLLLGESLFIREEQANILARVTPANSFLEEMKXHLRECMEE 60
QY 61 TCSVEAREVFEDSKTNEFNWYKDGDCETSPCQNGKCKDGLGEYTCCLGFEGRN 120
Db 61 TCSVEAREVFEDSKTNEFNWYKDGDCETSPCQNGKCKDGLGEYTCCLGFEGRN 120
QY 121 CELFTRKLCSLDNGDCQFCHEEQNSVVCSCARGYTLADNGKACITGYPGCKQTLERR 180
Db 121 CELFTRKLCSLDNGDCQFCHEEQNSVVCSCARGYTLADNGKACITGYPGCKQTLERR 180
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLRIVGGQ 240
Db 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLRIVGGQ 240
QY 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGE 300
Db 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGE 300
QY 301 AVHEVEVVIKHNRTKETDYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKGI 360
Db 301 AVHEVEVVIKHNRTKETDYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKGI 360
QY 361 VSGFGRTHKGRQSTRKMLKLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDG 420
Db 361 VSGFGRTHKGRQSTRKMLKLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDG 420
QY 421 GPHVTRFKDITVFTGIVSWGSCARKGKGIYTKVTAFLKWIIDRSMTKTRGLPKAKSHAP 480
Db 421 GPHVTRFKDITVFTGIVSWGSCARKGKGIYTKVTAFLKWIIDRSMTKTRGLPKAKSHAP 480
QY 481 VITSSPLK 488
Db 481 VITSSPLK 488

RESULT 4

US-10-360-101-233
; Sequence 233, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: heavy chain sequence of factor X
US-10-360-101-233

Query Match 62.5%; Score 1646; DB 15; Length 309;
Best Local Similarity 99.7%; Pred. No. 8.7e-129;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 180 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLRIVGGQ 239
Db 1 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLRIVGGQ 60
QY 240 ECKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGE 299
Db 61 ECKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGE 120
QY 300 EAVHEVEVVIKHNRTKETDYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKGI 359
Db 121 EAVHEVEVVIKHNRTKETDYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKGI 180
QY 360 IVSGFGRTHKGRQSTRKMLKLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDG 419
Db 181 IVSGFGRTHKGRQSTRKMLKLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDG 240
QY 420 GPHVTRFKDITVFTGIVSWGSCARKGKGIYTKVTAFLKWIIDRSMTKTRGLPKAKSHAP 479
Db 241 GPHVTRFKDITVFTGIVSWGSCARKGKGIYTKVTAFLKWIIDRSMTKTRGLPKAKSHAP 300
QY 480 EVITSSPLK 488
Db 301 EVITSSPLK 309

RESULT 5

US-10-406-031-5
; Sequence 5, Application US/10406031
; Publication No. US20040043017A1
; GENERAL INFORMATION:
; APPLICANT: Masci, Paul Pantaleone
; APPLICANT: Lavin, Martin
; TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
; FILE REFERENCE: 15685-002001
; CURRENT APPLICATION NUMBER: US/10/406,031
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: AU 2003901033
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: AU PSI483
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Oxyuranus scutellatus

Db 121 CERVLYKSCRVDNGNCWHFCKPQVNDIQCSAEGYLLGEGHSCVAGGNFSCGRNIKTEN 180
Qy 181 KRSVAQATSSSGEAPDSITWKPYDAALDPTENPFDLLDNQOQPERGNNLTRIVGGQE 240
Db 181 KREAS-----LPDFV--QSQNATLLKSDNP-----SPD-----IRIVNGMD 215
Qy 241 CKDGBCPQALLINEENEGFCGGTILSEFYILTAACHLYQAKFKYRVGDRNTEQEGGE 300
Db 216 CKLGECPQAVLVDEKSGVFCGGTILSPIVILTRAHCINQTEKISVVGEIDKSRVETGH 275
Qy 301 AVHEVEVVIKHNRTKE-----TYDPDIAVLRLKTPITFRMNVAPACLPED 347
Db 276 LL-SVDKIYVHKHVPVPPKGYKFEKFDLSYDYDIAIQMKTPIQFSENVVPACLPTAD 334
Qy 348 WAESTLMTQKTGIYSGFRTHKGRQSTRKMLKLEVPYVDRNSCKLSSSFIITQNMFCAGY 407
Db 335 PANQVLMKQDFGIISGGRITFEKPKNTLVKLVFPYVDRHTCMWSESPITPTMFCAGY 394
Qy 408 DTQOEDACQSDGGPHVTRFKDYTFVTGIVSWGESCARKGYIYTKVTAFLKWDIRSMK 467
Db 395 DTLPRDACQSDGGPHITAYRDTHTFITGIVSWGEGCAKGYIYTKVSKFILWIKRMR 454
Qy 468 TRGLPKAKS 476
Db 455 QK-LPSTES 462

RESULT 8
US-10-406-031-17
; Sequence 17, Application US/10406031
; Publication No. US20040043017A1
; GENERAL INFORMATION:
; APPLICANT: Masci, Paul Pantaleone
; APPLICANT: De Jersey, John
; APPLICANT: Lavin, Martin
; TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
; FILE REFERENCE: 15685-002001
; CURRENT APPLICATION NUMBER: US/10/406,031
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: AU 2003901033
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: AU PS1483
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Tropidechis carinatus
US-10-406-031-17

Query Match 46.4%; Score 1223; DB 12; Length 455;
Best Local Similarity 48.5%; Pred. No. 2.3e-93;
Matches 233; Conservative 70; Mismatches 141; Indels 36; Gaps 6;
Qy 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLEEMKKGHLERECME 60
Db 1 MAPQLLLCLITLFLWSLPEASNVFLKSKVANRFLQRTKESNLSLFEIRPGNIERECIE 60
Qy 61 TCSYEAREVEFEDSKTNEFWNKYKDGQCTSPCQNGKCKDGLGEYTCCTLEGPEGN 120
Db 61 KCSKEAREVEFEDNEKTETFWNVYVDGQCSNPFCHYRGCTCKDGGISYTCCLPNYEGN 120
Qy 121 CELFTRKLCSDNGDCQFCHQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180
Db 121 CEKVLQSCRVDNGNCWHFCKRVQSEFQCCASRYLGVGDGHSVAGGDFSCGRNIKARN 180
Qy 181 KRSVAQATSSSGEAPDSITWKPYDAALDPTENPFDLLDNQOQPERGNNLTRIVGGQE 240
Db 181 KREAS-----LPDFV--QSQNATLLKSDNP-----SPD-----IRIVNGMD 215
Qy 241 CKDGBCPQALLINEENEGFCGGTILSEFYILTAACHLYQAKFKYRVGDRNTEQEGGE 300
Db 216 CKLGECPQAVLVDEKSGVFCGGTILSPIVILTRAHCINQTEKISVVGEIDKSRVETGH 275
Qy 301 AVHEVEVVIKHNRTKE-----TYDPDIAVLRLKTPITFRMNVAPACLPED 347
Db 276 LL-SVDKIYVHKHVPVPPKGYKFEKFDLSYDYDIAIQMKTPIQFSENVVPACLPTAD 334
Qy 348 WAESTLMTQKTGIYSGFRTHKGRQSTRKMLKLEVPYVDRNSCKLSSSFIITQNMFCAGY 407
Db 335 PANQVLMKQDFGIISGGRITFEKPKNTLVKLVFPYVDRHTCMWSESPITPTMFCAGY 394
Qy 408 DTQOEDACQSDGGPHVTRFKDYTFVTGIVSWGESCARKGYIYTKVTAFLKWDIRSMK 467
Db 395 DTLPRDACQSDGGPHITAYRDTHTFITGIVSWGEGCAKGYIYTKVSKFILWIKRMR 454
Qy 468 TRGLPKAKS 476
Db 455 QK-LPSTES 462

Db 216 CKLGECPQAVLVINEKEVFCGGTILSPIHLVTRAHCINQTKSVSVIVGEIDISRKETR 275
Qy 301 --AVHEVEVVIK-----HNRFTKETDYDFDIAVLRLKTPITFRMNVAPACLPEDWA 349
Db 276 LLSVDKIYVHKHVPVPPKGYKFEKFDLSYDYDIAIQMKTPIQFSENVVPACLPTADFA 335
Qy 350 ESTLMTQKTGIYSGFRTHKGRQSTRKMLKLEVPYVDRNSCKLSSSFIITQNMFCAGYDT 409
Db 336 NEVLMKQDSGLVSGFRIQFKQPTNTLVKLVFPYVDRHTCMWSESPITPTMFCAGYDT 395
Qy 410 KQEDACQSDGGPHVTRFKDYTFVTGIVSWGESCARKGYIYTKVTAFLKWDIRSMKTR 469
Db 396 LPQDACQSDGGPHITAYRDTHTFITGIVSWGEGCAKGYIYTKVSKFILWIKRMR 455

RESULT 9
US-10-406-031-11
; Sequence 11, Application US/10406031
; Publication No. US20040043017A1
; GENERAL INFORMATION:
; APPLICANT: Masci, Paul Pantaleone
; APPLICANT: De Jersey, John
; APPLICANT: Lavin, Martin
; TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
; FILE REFERENCE: 15685-002001
; CURRENT APPLICATION NUMBER: US/10/406,031
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: AU 2003901033
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: AU PS1483
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Pseudechis porphyriacus
US-10-406-031-11

Query Match 46.4%; Score 1222; DB 12; Length 454;
Best Local Similarity 47.0%; Pred. No. 3e-93;
Matches 228; Conservative 75; Mismatches 148; Indels 34; Gaps 6;
Qy 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLEEMKKGHLERECME 60
Db 1 MAPQLLLCLITLFLWSLPEASNVFLKSKVANRFLQRTKESNLSLFEIRPGNIERECIE 60
Qy 61 TCSYEAREVEFEDSKTNEFWNKYKDGQCTSPCQNGKCKDGLGEYTCCTLEGPEGN 120
Db 61 KCSKEAREVEFEDNEKTETFWNVYVDGQCSNPFCHYRGCTCKDGGISYTCCLPNYEGN 120
Qy 121 CELFTRKLCSDNGDCQFCHQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180
Db 121 CEHLLFKSCRFNGNCWHFCKPVQNDTQCSAESYRLGDDGHSVAGGDFSCGRNIKARN 180
Qy 181 KRSVAQATSSSGEAPDSITWKPYDAALDPTENPFDLLDNQOQPERGNNLTRIVGGQE 240
Db 181 KREAS-----LPDFV--QSQNATLLKSDNP-----SPD-----IRIVNGMD 215
Qy 241 CKDGBCPQALLINEENEGFCGGTILSEFYILTAACHLYQAKFKYRVGDRNTEQEGGE 300
Db 216 CKLGECPQAVLVDEKSGVFCGGTILSPIVILTAACHITQSKHISVVGEIDISRKETH 275
Qy 301 AVHEVEVVIKHNRTKE-----TYDPDIAVLRLKTPITFRMNVAPACLPED 347
Db 276 LL-SVDKIYVHKHVPVPPKGYKFEKFDLSYDYDIAIQMKTPIQFSENVVPACLPTAD 334
Qy 348 WAESTLMTQKTGIYSGFRTHKGRQSTRKMLKLEVPYVDRNSCKLSSSFIITQNMFCAGYDT 409
Db 335 ISGFGRTHKGRQSTRKMLKLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQDADACQSDG 394
Qy 421 GPHVTRFKDYTFVTGIVSWGESCARKGYIYTKVTAFLKWDIRSMKTRGLPKAKSHAPE 480


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Db      395 GPHITAYRDTHTFITGIISWGEGCAKKGKGYGVYVTVKSNFIPWIKAVM-----RKHPQS 446
QY      481 VITSS 485
Db      447 TESST 451

RESULT 10
US-10-406-031-14
; Sequence 14, Application US/10406031
; Publication No. US2004043017A1
; GENERAL INFORMATION:
; APPLICANT: Masci, Paul Pantaleone
; APPLICANT: De Jersey, John
; APPLICANT: Lavin, Martin
; TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
; FILE REFERENCE: 15685-002001
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: AU 2003901033
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: AU 2003901033
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: No. US20040043017A1elechis scutatus
US-10-406-031-14

Query Match      46.2%; Score 1216; DB 12; Length 453;
Best Local Similarity 48.6%; Pred No. 9.5e-93;
Matches 233; Conservative 69; Mismatches 141; Indels 36; Gaps 6;

QY      1 MGRPLHLVLSASLACLLGLLSLPIRREQANNILARVTRANSFLEMKKGLHRECMEE 60
Db      1 MAPQLLLCLILFLWSLPAESNVLKSKVANRFLQRTKRSNLSFELIRPCNIERECIEE 60
QY      61 TCSYEBAREVFEDSKTNEFWNKYKDGQCETSPQNGCKGCKDGLGEVYTCCLGEPGKN 120
Db      61 KSKKEBARVFEDNEKTETFMNVYVDGQCSNPNCHYRGTCCKDGISYTCCLPNYEGKN 120
QY      121 CELFTRKLSLNGDCDFCHEEQNSVVCSCARGYTLADNGKACIPTGPVPCGKQTLRR 180
Db      121 CEKVLIFKSCRAFNGNWHFCRKVQSETQCSAESYLLGVGDGHS CVABGDFSCGGRNIKARN 180
QY      181 KRSVAQATSSGSEAPDSITWKPYDAADLDPTENPDLDDFNQTOPERGDNNILTVGGQE 240
Db      181 KREAS-----LPDFV--QSKATVLKKSNDP-----SPD-----IRVNGMD 215
QY      241 CKDGECPQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEEGGE 300
Db      216 CKLGECPQAVLINEKEGEVFCGGTILSPHVLTAHCINQTKSVSVIVGEIDISRKETRR 275
QY      301 AHEVEVVIKHNFT-----KEYDDEIAVLRLKTPITFMNVVAPACILPERDWAEE 350
Db      276 LL-SVDKIYVHKKFPNPNSSYYQNIDRFAYDYDIAIRMKTPIQFSENVVAPCLPTADFAK 334
QY      351 STLMTQKTGIVSGFGRTHKEGRQSTRLKMLEVPYVYDRNSCKLSSSFIITQNMFCAGYDTK 410
Db      335 EVLMKQDSGIVSGFGRGTQSIGYTSNLIKVIIVPYVDHRTCMLSNFRITQNMFCAGYDIL 394
QY      411 QEDACGDSGGGPHVTRPKDTYFTVGIWNGESCARKKGYGIVTKVTAFLKWDIRSMKTR 469
Db      395 PDACQCGDSGGPHITAYGDTHTFVTGIISWGEGCAKKGKGYGVYVTVKSNFIPWIKMSLK 453

RESULT 11
US-10-406-031-31
; Sequence 31, Application US/10406031
; Publication No. US20040043017A1
; GENERAL INFORMATION:

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; APPLICANT: Masci, Paul Pantaleone
; APPLICANT: De Jersey, John
; APPLICANT: Lavin, Martin
; TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
; FILE REFERENCE: 15685-002001
; CURRENT APPLICATION NUMBER: US/10/406,031
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: AU 2003901033
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: AU PSI483
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Tropidochis carinatus
US-10-406-031-31

Query Match      43.1%; Score 1135.5; DB 12; Length 376;
Best Local Similarity 47.7%; Pred. No. 3.8e-86;
Matches 209; Conservative 55; Mismatches 103; Indels 71; Gaps 3;

QY      41 ANSFLEEMKKGHLRECEMERTCSYEAREVFEDSKTNEFWNKYKDGQCETSPQNGCK 100
Db      1 SNLSFELIRPCNIERECIEKSKKEAREVFEDNEKTETFMNVYVDGQCSNPNCHYRG 60
QY      101 CKDGLGEVYTCCLGEPGKNCLEFTRKLSLNGDCDFCHEEQNSVVCSCARGYTLADN 150
Db      61 CKDGISYTCCLPNYEGKCKEVLQYQSCRVDNGNCHWHFCRKVQSETQCSAESYRLGD 120
QY      161 GKACIPTGPVPCGKQTLERRKRSVAQATSSGSEAPDSITWKPYDAADLDPTENPDLDD 220
Db      121 GHSCVAEGDFSCGRNIKARNK-----141
QY      221 NQTOPERGDNNILTVGGQCKDGECPQALLINEENEGFCGGTILSEFYILTAHCLYQ 280
Db      142 -----INVGMCKLGECPQAVLINEKEGEVFCGGTILSPHVLTAHCINQ 187
QY      281 AKRFKRVGDRNTEQEEGGAHVEVVIK-----HNRFTKETYDFDIAVLRLKTP 331
Db      188 TKSVK-----ETRLLSVDKIYVHTKFEVPPNYYVHONFDRVAYDYDIAIRMKTP 238
QY      332 ITRFMNVVAPACILPERDWAESTLMTQKTGIVSGFGRTHKEGRQSTRLKMLEVPYVYDRNSCK 391
Db      239 IQFSENVVAPACILPTADPANEVLKMKQDSGIVSGFGRIQKQPTNLTKLVIIVPYVDHRTCM 298
QY      392 LSSSFIITQNMFCAGYDTKQEDACQDSGGPHVTRPKDTYFTVGIWNGESCARKKGYGI 451
Db      299 LSSDFRITQNMFCAGYDTLPQDACQDSGGPHITAYRDTHTFVTGIISWGEGCAKKGKYG 358
QY      452 YTKVTAFLKWDIRSMKTR 469
Db      359 YTKVSKFIPWIKMSLK 376

RESULT 12
US-09-684-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: USFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461

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Query Match
Best Local Similarity 39.5%; Score 1041.5; DB 9; Length 461;
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

9 LLSASLAGLLILGE-SLFIRREOANNILARVTRANS-FLEEMKKGHLERECMEETCSYEE 66
14 LITICLLGYLLSAECTVFLDENANKILNRPKNYNSKLEEFVQGNLERECMEEKCSFEE 73
67 AREVFEDSKTNEFWNKYKDGOCETSPCONQCKGKGLGEYTCCTLEGEGKNCCLFTR 126
74 AREVFENTERTEFWKQYVDGOCESNPLNGGSKDDINSYECWCFPGFEGKNCCLDV- 132
127 KLCSLDNGDCDOFC-HEQNSVVCSCARGYTLADNGKACIPTGYPCKGKOTLERRKRSVA 185
133 -TCNKNKRCQECQCKNSADNKVVCSTEGYRLAENQKSCPEPAVFPFCGRVSVSQ----TS 187
186 QATSSGSEAPDSITWPKFYDAADLPDENPFLDNPOTQPERGDNNTLRIVGGQCKDGE 245
188 KLTRAFAVFPD-----VDYVNSTEAETILD-----NITQSTQSFNDFTRVGGEDAKPGQ 237
246 CPWQALLINEENEGPCGGTILSEFYILTAACHLYQAKRFKVRVGDNRNTEOEGGEAVHEV 305
238 FFWQVVL-NGKVDAPCGSIVNEKVIWTAACHVETGKIVTVAAGEHNIETEHTOKRNV 296
306 EVVIKHNRTK--ETYPDIAVLRLKTPITFRMNVAPACILPERDWAESTLMTQKTGIVSG 363
297 IRIIPHNYNAAINKYNHDIALLDELPLVNSYVTPICIADEYNT-NIFLKFGSGYVSG 355
364 FGRTHKGRQSTRMLKLEVPVDRNSCKLSSFIITONMFCAGYDTKQEDACOGDSGGPH 423
297 IRIIPHNYNAAINKYNHDIALLDELPLVNSYVTPICIADEYNT-NIFLKFGSGYVSG 355
364 FGRTHKGRQSTRMLKLEVPVDRNSCKLSSFIITONMFCAGYDTKQEDACOGDSGGPH 423
356 WGRVTHKGRSALVQLYRLVPLVDRATCLRSTKFTIYNMFCAGFHEGGRDSCQDSDGGPH 415
424 VTRFKDTYFTVTVGIVSWGSCARKGKGIYTKVTAFLKWDIDRSKM 467
416 VTEVEGTSFLTGIIISWGECAKMGKGIYTKVRYNWIKEKTK 459

RESULT 13

US-10-234-406-8
Sequence 8, Application US/10234406
Publication No. US20030109478A1
GENERAL INFORMATION:
APPLICANT: FEWEL, Jason G.
APPLICANT: MACLAUGHLIN, Fiona
APPLICANT: SMITH, Louis C.
APPLICANT: NICOL, Francois
APPLICANT: ROLLAND, Alain
TITLE OF INVENTION: NUCLEIC ACID FORMULATIONS FOR GENE DELIVERY AND METHODS OF USE
FILE REFERENCE: 54964.8303.US01
CURRENT APPLICATION NUMBER: US/10/234.406
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US 60/187,236
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 60/261,751
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: PCT/US01/06953
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 461
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Expression plasmid pBN1645 having codon optimized sequence encoding ng for human coagulation factor IX (786) ... (2171).

Query Match 39.5%; Score 1041.5; DB 14; Length 461;

Best Local Similarity 44.8%; Pred. No. 3.3e-78;
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

9 LLSASLAGLLILGE-SLFIRREOANNILARVTRANS-FLEEMKKGHLERECMEETCSYEE 66
14 LITICLLGYLLSAECTVFLDENANKILNRPKNYNSKLEEFVQGNLERECMEEKCSFEE 73
67 AREVFEDSKTNEFWNKYKDGOCETSPCONQCKGKGLGEYTCCTLEGEGKNCCLFTR 126
74 AREVFENTERTEFWKQYVDGOCESNPLNGGSKDDINSYECWCFPGFEGKNCCLDV- 132
127 KLCSLDNGDCDOFC-HEQNSVVCSCARGYTLADNGKACIPTGYPCKGKOTLERRKRSVA 185
133 -TCNKNKRCQECQCKNSADNKVVCSTEGYRLAENQKSCPEPAVFPFCGRVSVSQ----TS 187
186 QATSSGSEAPDSITWPKFYDAADLPDENPFLDNPOTQPERGDNNTLRIVGGQCKDGE 245
188 KLTRAFAVFPD-----VDYVNSTEAETILD-----NITQSTQSFNDFTRVGGEDAKPGQ 237
246 CPWQALLINEENEGPCGGTILSEFYILTAACHLYQAKRFKVRVGDNRNTEOEGGEAVHEV 305
238 FFWQVVL-NGKVDAPCGSIVNEKVIWTAACHVETGKIVTVAAGEHNIETEHTOKRNV 296
306 EVVIKHNRTK--ETYPDIAVLRLKTPITFRMNVAPACILPERDWAESTLMTQKTGIVSG 363
297 IRIIPHNYNAAINKYNHDIALLDELPLVNSYVTPICIADEYNT-NIFLKFGSGYVSG 355
364 FGRTHKGRQSTRMLKLEVPVDRNSCKLSSFIITONMFCAGYDTKQEDACOGDSGGPH 423
356 WGRVTHKGRSALVQLYRLVPLVDRATCLRSTKFTIYNMFCAGFHEGGRDSCQDSDGGPH 415
424 VTRFKDTYFTVTVGIVSWGSCARKGKGIYTKVTAFLKWDIDRSKM 467
416 VTEVEGTSFLTGIIISWGECAKMGKGIYTKVRYNWIKEKTK 459

RESULT 14

US-10-038-854-92
Sequence 92, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vernet, Corine
APPLICANT: Eisen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uziel M
APPLICANT: Shmets, Richard A
APPLICANT: Tchernev, Velizar
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Rameesh
APPLICANT: Patturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangolli, Esha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928

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; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 92
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-92

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Query Match      39.5%; Score 1041.5; DB 16; Length 461;
Best Local Similarity 44.8%; Pred. No. 3.3e-78;
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

QY 9 LLSASLAGLLGGE-SLFFIRREQANNILARVTRANS-FLEEMKKGHLERECMEETCSYEE 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 LITICLLGYLLSABCTVFLDHENANKILNRPKYNKGLSEFFVQGNLERECMEKCSFEE 73
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 AREVPEDSKTNEFWNKYKDGQCTSPQONQKCKDGLGEYTCCTLEGEGKNCCLFTR 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 AREVPENTERTEFWKQYVDGQCESNPLNGSGCKDDINSYECWCPFGFEGKNCCLDV- 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 KLCSLDNGDCDQFC-HEEQNSVVCSCARGYTLADNGKACIPTGPGCKOTLERRKESVA 185
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 -TCNKNKRCQFCCKNSADNKNVCSCTEGYRLAENQKSCPEAVPFGCRVSVSQ- ---TS 187
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 186 QATSSSGEAPDSITWKPYDAADLDPENPFLLDFNQTOPERGNLNLTRIVGGQCKDGE 245
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 KLTRAFAVFPD-----VDYVNSTEAETILD-----NITQSTQSFNDFTRVVGSDAKPGQ 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 CPWQALLINEEGPCGGTILSEFYILTAACHLYQAKFKVYVGRDNTQEGGEAVHEV 305
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FPMQVVL-NGKVDAPCGGSIVNEKVIITAAHCVEVGKIIIVVAGEHNIETEHEQKENV 296
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 306 EVVIKHNRFK--ETDPIAVLRKTPITFRMNVAPACLPERDWAESTLMTQKTGIVSG 363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 IRIIPHNNAINKYNHDIALLDEPLVLSYVTRICIADKEYT-NIFLKFGSGYVSG 355
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 364 FGRTHEKRGOSTRLKMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGPH 423
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 WGRVFHKGRSALVQLYLRVPLVDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQDGGPH 415
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 424 VTRFKDTYFVTGIVSWGESCARKGKIYTKVTAFLKWDIRSMK 467
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 416 VTEVEGTSFLTGIISWGEBCAMKKGKIYTKVSRVYVNNWIKETK 459
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```

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RESULT 15
US-10-239-498A-5
; Sequence 5, Application US/10239498A
; Publication No. US2004002333A1
; GENERAL INFORMATION:
; APPLICANT: Hauser, Charlotte
; APPLICANT: Horster, Andrea
; APPLICANT: Schroder, Carola

```

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; APPLICANT: Lehnere, Michael
; TITLE OF INVENTION: Production of Recombinant Blood Clotting Factors in
; FILE REFERENCE: 80977.0001
; CURRENT APPLICATION NUMBER: US/10/239,498A
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/03220
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-498A-5

Query Match      39.5%; Score 1041.5; DB 16; Length 461;
Best Local Similarity 44.8%; Pred. No. 3.3e-78;
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

QY 9 LLSASLAGLLGGE-SLFFIRREQANNILARVTRANS-FLEEMKKGHLERECMEETCSYEE 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 LITICLLGYLLSABCTVFLDHENANKILNRPKYNKGLSEFFVQGNLERECMEKCSFEE 73
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 AREVPEDSKTNEFWNKYKDGQCTSPQONQKCKDGLGEYTCCTLEGEGKNCCLFTR 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 AREVPENTERTEFWKQYVDGQCESNPLNGSGCKDDINSYECWCPFGFEGKNCCLDV- 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 KLCSLDNGDCDQFC-HEEQNSVVCSCARGYTLADNGKACIPTGPGCKOTLERRKESVA 185
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 -TCNKNKRCQFCCKNSADNKNVCSCTEGYRLAENQKSCPEAVPFGCRVSVSQ- ---TS 187
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 186 QATSSSGEAPDSITWKPYDAADLDPENPFLLDFNQTOPERGNLNLTRIVGGQCKDGE 245
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 KLTRAFAVFPD-----VDYVNSTEAETILD-----NITQSTQSFNDFTRVVGSDAKPGQ 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 CPWQALLINEEGPCGGTILSEFYILTAACHLYQAKFKVYVGRDNTQEGGEAVHEV 305
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FPMQVVL-NGKVDAPCGGSIVNEKVIITAAHCVEVGKIIIVVAGEHNIETEHEQKENV 296
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 306 EVVIKHNRFK--ETDPIAVLRKTPITFRMNVAPACLPERDWAESTLMTQKTGIVSG 363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 IRIIPHNNAINKYNHDIALLDEPLVLSYVTRICIADKEYT-NIFLKFGSGYVSG 355
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 364 FGRTHEKRGOSTRLKMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGPH 423
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 WGRVFHKGRSALVQLYLRVPLVDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQDGGPH 415
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 424 VTRFKDTYFVTGIVSWGESCARKGKIYTKVTAFLKWDIRSMK 467
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 416 VTEVEGTSFLTGIISWGEBCAMKKGKIYTKVSRVYVNNWIKETK 459
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: April 14, 2004, 15:46:09
Job time : 48 secs

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> O <
O | / O IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "hopel-ags" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
hopel (AA) ID hopel AA preliminary pattern
1 followed by
2 e
3 q or s or h or y or e
4 s or q or i or t or n or p
5 f or t or s or p or l or i
6 n or s or k or m or t or p
7 d or k or t or e
8 f or l or r or i
9 t or s or n
0 r
1 i or v or a

Selected data banks and files:
Data bank: A-GeneSeq 35.2, all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact Indirect file
Find non-matching hits only No Sequence or key file
Report key used Yes List of hits
Display full annotations Yes Hit display
Sequence context 10 Name and annotations

File Options:
Nucleic acid code matching Exact Indirect file
Find non-matching hits only No Sequence or key file
Report key used Yes List of hits
Display full annotations Yes Hit display
Sequence context 10 Name and annotations

Run mode Batch
Time to start comparison now
Notify at end of run No

-- Run Parameters --

1 match found in sequence:
R30729 ; p100 protein from human herpes virus type 6.
(from "A-GeneSeq 35.2")
ID R30729 standard; Protein; 870 AA.
AC R30729
DE p100 protein from human herpes virus type 6.
KW antibodies; monoclonal antibody; ELISA assays; CMV; cytomegalovirus.
OS Human herpes virus type 6.
PN EP-524421-A.
PD 27-JAN-1993.
PF 15-JUN-1992; 110047.
PR 08-JUL-1991; EP-111338.
PA (BEHW) BEHRINGERWEGE AG.
PI Fleckenstein B, Neipel F;
DR WPI; 93-028531/04.
DE R30729.
PT Human herpes virus type 6 protein p100 DNA sequence - useful in
PT prophylaxis, treatment and differential diagnosis of human herpes
PT virus-6 infections
PS Claim 1; Page 12; 25pp; English.
CC This sequence is the p100 protein from human herpes virus type 6.
CC The protein and antibodies to it can be used for treatment or
CC prevention of HHV-6 infections. The DNA, protein and Ab are also
CC useful in eg. ELISA assays esp. for differentiating between HHV-6
CC and cytomegalovirus infections. These assays are more sensitive

```

```

CC and specific than immunofluorescence methods currently used.
SQ Sequence 870 AA.
SQ 43 A; 42 R; 67 N; 69 D; 0 B; 1 C; 33 Q; 57 E; 0 Z; 54 G; 16 H;
SQ 42 I; 94 L; 63 K; 17 W; 33 F; 35 P; 86 S; 46 T; 8 W; 15 Y; 49 V;
Found using 'hopel' (new.key)

...

110 emftnkefegsfedlnrallrlgnfkW
120 129
...

1 match found in sequence:
R42456 ; Enzyme involved in eicosapentaenoic acid (EPA) synthesis.
(from "A-GeneSeq 35.2")
ID R42456 standard; Protein; 543 AA.
AC R42456;
DE 27-MAY-1994 (first entry)
DE Enzyme involved in eicosapentaenoic acid (EPA) synthesis.
KW EPA; eicosapentaenoic acid synthetase; drug; anticoagulant;
KW hypolipemic; hypoglycemic; antihypertensive; anticancer; pesticide;
KW foodstuff; additive.
KW Shewanella putrefaciens.
OS WO9323545-A.
PN 25-NOV-1993.
PF 14-MAY-1993; J00641.
PR 15-MAY-1992; JP-147945.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PI Kato S, Kondo K, Yamada A, Yazawa K;
DR WPI; 93-38577/48.
DE N-PSDB; Q51128.
PT Gene coding for eicosa-penta:enoic acid synthetase - is isolated
PT from Pseudomonas, Alteromonas or Shewanella and used for
PT recombinant prodn. of eicosa-penta:enoic acid
PS Claim 10; Page 91-94; 106pp; Japanese.
CC EPA is useful as a drug, having anticoagulant, hypolipemic,
CC hypoglycemic, antihypertensive and anticancer activity. It is also
CC a pesticide and is useful as a nutritional foodstuff and animal feed
CC additive.
SQ Sequence 543 AA;
SQ 69 A; 28 R; 25 N; 26 D; 0 B; 4 C; 24 Q; 33 E; 0 Z; 41 G; 9 H;
SQ 27 I; 46 L; 25 K; 20 M; 17 F; 26 P; 30 S; 28 T; 8 W; 19 Y; 38 V;
Found using 'hopel' (new.key)

...

20 snisfdvqmegqklkdfaracyvvnhadg
30 39
...

1 match found in sequence:
R99465 ; Biosynthetic enzyme of icosapentaenoic acid synthase.
(from "A-GeneSeq 35.2")
ID R99465 standard; Protein; 543 AA.
AC R99465;
DE 30-JAN-1997 (first entry)
DE Biosynthetic enzyme of icosapentaenoic acid synthase.
KW Icosapentaenoic acid synthase; EPA; drugs; agrochemicals;
KW foodstuffs; animal feed; lipid balance correction; antihypertensive;
KW anti-inflammatory; anticancer agent.
KW Shewanella putrefaciens.
OS WO9621735-A1.
PN 18-JUL-1996.
PF 12-JAN-1996; J00030.
PR 13-JAN-1995; JP-004299.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PI Kato S, Kondo K, Yamada A, Yazawa K;

```

DR WPI; 96-342288/34.
DR N-PSDB; T34137.
PT Production of eicosapentaenoic acid using transformed E. coli - uses
PT DNA coding for eicosapentaenoic acid synthase derived from Shewanella
PT strain
PS Claim 7; Page 128-131; 145pp; English.
CC The DNA sequence (T34137) which encodes the biosynthetic enzymes of
CC eicosapentaenoic acid (EPA) can be used to transform Escherichia coli.
CC The DNA sequence allows efficient microbial production of EPA, which
CC is a raw material for drugs, agrochemicals, foods and animal
CC feedstuffs. EPA is also useful for lipid balance correction and as
CC an antihypertensive, antiinflammatory and anticancer agent.
SQ Sequence 543 AA;
SQ 69 A; 28 R; 25 N; 26 D; 0 B; 4 C; 24 Q; 33 E; 0 Z; 41 G; 9 H;
SQ 27 I; 46 L; 25 K; 20 M; 17 F; 26 P; 30 S; 28 T; 8 W; 19 Y; 38 V;
Found using 'hopel' (new.key)

...

20 snisfdvqvmegqikdfsracyvvnhadhg
30
39

...

1 match found in sequence:
W37053 ; S. putrefaciens EPO biosynthesis gene cluster ORF9 product.
(from "A-Geneseq 35.2")
ID W37053 standard; Protein; 543 AA.
AC W37053
DT 03-JUL-1998 (first entry)
DE S. putrefaciens EPO biosynthesis gene cluster ORF9 product.
KW SCRC-2874; FERM BP-1625; eicosapentaenoic acid; EPA;
KW biosynthesis gene cluster; synthetase.
OS Shewanella putrefaciens.
PN W09801565-A1.
PD 15-JAN-1998.
PF 09-JUN-1997; J02371.
PR 10-JUL-1996; JP-180845.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PI Kato S, Kondo K, Yamada A, Yazawa K;
DR WPI; 98-101060/09.
DR N-PSDB; V00503.
PT Eicosapentaenoic acid produced by culture of transformed Escherichia
PT coli - containing an eicosapentaenoic acid synthetase gene derived
PT from the marine microorganism Shewanella
PS Example 1; Pages 93-97; 110pp; Japanese.
CC The present sequence is encoded by the Shewanella putrefaciens
CC SCRC-2874 (FERM BP-1625) eicosapentaenoic acid (EPA) biosynthesis
CC gene cluster.
CC A novel EPA (useful in drugs, pesticides, foods and feedstuffs) is
CC encoded by synthetase enzyme gene sequences comprising parts of the
CC full sequence of the synthetase gene from the marine microorganism
CC S. putrefaciens SCRC-2874 (FERM BP-1625), in which at least 1 of
CC the 9 open reading frames (ORF) (numbered 2-10) in the gene have
CC been deleted. In particular the gene sequences comprising the
CC following parts of the full gene:
CC (1) bases 8081-9441, 12314-13084 and 13889-32520;
CC (2) bases 8081-9441, 12314-13084, 13889-32520 and 34627-35559;
CC (3) bases 8081-9441, 12314-13084 and 13889-35559;
CC (4) bases 8081-9441, 9681-13084 and 13889-32520;
CC (5) bases 8081-9441, 9681-13084, 13889-32520 and 34627-35564; and
CC (6) bases 8081-9441, 9681-13084 and 13889-35564, are claimed.
SQ Sequence 543 AA;
SQ 69 A; 28 R; 25 N; 26 D; 0 B; 4 C; 24 Q; 33 E; 0 Z; 41 G; 9 H;
SQ 27 I; 46 L; 25 K; 20 M; 17 F; 26 P; 30 S; 28 T; 8 W; 19 Y; 38 V;
Found using 'hopel' (new.key)

...

20 snisfdvqvmegqikdfsracyvvnhadhg

...
30 39
-- Search Statistics --
Times: CPU
00:00:20.03
Total Elapsed
00:00:23.00
Number of sequences searched: 170751
Number of sequence hits: 4
Number of separate matches: 4
Number of sequence hits saved: 0

FINDPATTERNS on genesep: * allowing 0 mismatches

1 E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R,I) (T,S,N,R) 1
1 AAR30729 ck: 500 len: 870 ! Aar30729 p100 protein from human herpes vir 1
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R) 1
E(S) (O) (L) (K) (D) (F) (S)R(A) 1
120: NKEKF ESQSDINRA LLRLG 1
1 AAR42456 ck: 3609 len: 543 ! Aar42456 Enzyme involved in eicosapentaenoic 1
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R) 1
E(O) (O) (L) (K) (D) (F) (S)R(A) 1
30: DVQVM EQQLKDFSA CYVNV 1
1 AAR99465 ck: 3609 len: 543 ! Aar99465 Biosynthetic enzyme of icosapentae 1
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R) 1
E(O) (O) (L) (K) (D) (F) (S)R(A) 1
30: DVQVM EQQLKDFSA CYVNV 1
1 AAW37053 ck: 3609 len: 543 ! Aaw37053 S. putrefaciens EPO biosynthesis g 1
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R) 1
E(O) (O) (L) (K) (D) (F) (S)R(A) 1
30: DVQVM EQQLKDFSA CYVNV 1
1 AAW89403 ck: 3609 len: 543 ! Aaw89403 S. putrefaciens PKS-like cluster C 1
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R) 1
E(O) (O) (L) (K) (D) (F) (S)R(A) 1
30: DVQVM EQQLKDFSA CYVNV 1
1 AAB10470 ck: 3609 len: 543 ! Aab10470 Shewanella putrefaciens PKS protei 1
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R) 1
E(O) (O) (L) (K) (D) (F) (S)R(A) 1
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1 AAG52216 ck: 7182 len: 274 ! Aag52216 Arabidopsis thaliana protein fragm 1
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111: QQVNP EENSNTLN RV NLGEQ 1
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E(E) (N) (S) (N) (T) (L) (N)R(V) 1
45: QQVNP EENSNTLN RV NLGEQ 1
1 AAG64458 ck: 9499 len: 542 ! Aag64458 S. putrefaciens eicosapentanoic ac 1
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R) 1
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Databases searched:

EMBL, Release 2.0, Released on 29Jan2004, Formatted on 12Feb2004

Total finds: 14
Total length: 282,547,505
Total sequences: 1,586,107
CPU time: 11:19.35

Number in blue corresponds
to citation.

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AC AAB10470;
XX
DT 11-DEC-2000 (first entry)
XX
DE Shewanella putrefaciens PKS protein ORF9.
XX
XX PKS pathway; polyunsaturated long chain fatty acid; plant; transgenic;
KW polyketide-like synthesis; PUFA; dietary supplement; intravenous feeding;
KW malnutrition; cooking oil; cooking fat; margarine;
KW docosahexenoic acid production; eicosapentenoic acid production.
XX
XX Shewanella putrefaciens.
OS
XX
XX
XX WO2000042195-A2.
XX
XX 20-JUL-2000.
XX
XX 14-JAN-2000; 2000WO-US000956.
XX
XX 14-JAN-1999; 99US-00231899.
XX
XX (CALJ) CALGENE LLC.
XX
XX Facciotti D, Metz JG, Lassner M;
XX
XX WPI; 2000-476063/41.
XX
XX New DNA sequences encoding for polyketide (PK)-like synthesis pathway
PT Genes from Shewanella, Vibrio and Schizochthrium, useful for creating
PT transgenic plants that express poly-unsaturated long chain fatty acids.
XX
XX Example 1; Fig 4J; 302pp; English.
XX
XX This invention describes novel DNA sequences encoding for polyketide (PK)
XX -like synthesis (PKS-like) pathway genes from Shewanella, Vibrio and
XX Schizochthrium. The nucleic acids are useful for isolating related
XX molecules or in methods to detect organisms expressing the PKS-like
XX genes. They are also useful for creating transgenic plants that express
XX poly-unsaturated long chain fatty acids. The poly-unsaturated long chain
XX fatty acids produced recombinantly are useful as dietary supplements for
XX patients undergoing intravenous feeding or for preventing or treating
XX malnutrition. The poly-unsaturated long chain fatty acids can also be
XX incorporated into cooking oils, fats or margarine formulated so that in
XX normal use the recipient receives a desired amount of poly-unsaturated
XX long chain fatty acids. The nucleic acids are also useful in large scale
XX production of docosahexenoic acid and eicosapentenoic acid, and for the
XX modification of the fatty acid profile of host cells and edible plant
XX tissues and/or plant parts. Transgenic production of polyunsaturated
XX fatty acids in particular host cells allows quicker purification from
XX natural sources such as fish or plants. This sequence represents the
XX Shewanella putrefaciens PKS protein cluster ORF9 which is described in
XX the method of the invention
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Wol 2004

TOIG of: aag52216 check: 7182 from: 1 to: 274
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DT 18-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 56352.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
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XX EP1033405-A2.
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XX 06-SEP-2000.
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XX (CERE-) CERES INC. ; XX
Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME ; PI
Zheng L, Dumas J ; PI
XX WPI: 2000-507395/46. ; XX
XX N-FSDS; AAC50845. ; XX
XX New sequence determined DNA fragments (SDFs) from different plant ; PT
species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters, ; PT
protein coding sequences, untranslated regions, or as 3' termination ; PT
sequences. ; PT
XX Claim 19; SEQ ID NO 66352; 344pp + Sequence Listing; English. ; PS
XX The present sequence is a putative protein fragment from Arabidopsis ; CC
thaliana. Its coding sequence was isolated by carrying out RT-PCR on all ; CC
of the mRNA obtained from the plant, and creating a cDNA library which ; CC
could then be sequenced, allowing the putative protein sequence(s) to be ; CC
obtained. This sequence may be useful for protein identification and for ; CC
aiding in the elucidation of signal transduction and metabolic pathways. ; CC
XX Its coding sequence has a use in the control of gene expression as a ; CC
promoter, coding sequence, 3'UTR or termination sequence, for controlling ; CC
the behaviour of a gene within the chromosome, as a tool for use in ; CC
genetic mapping, including a use in hybridisation assays, for recognition ; CC
or isolation of similar DNA fragments, or for the identification of a ; CC
particular organism ; CC
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DT 18-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX (CERE-) CERES INC.
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX DR WPI; 2000-507395/46.
XX DR N-PSDB; AAC50846.
XX PS New sequence determined DNA fragments (SDFs) from different plant
XX PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
XX PT protein coding sequences, untranslated regions, or as 3' termination
XX PT sequences.
XX PS Claim 19; SEQ ID NO 66353; 344pp + Sequence Listing; English.
XX CC The present sequence is a putative protein fragment from Arabidopsis
XX CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
XX CC of the mRNA obtained from the plant, and creating a cDNA library which
XX CC could then be sequenced, allowing the putative protein sequence(s) to be
XX CC obtained. This sequence may be useful for protein identification and for
XX CC aiding in the elucidation of signal transduction and metabolic pathways.
XX CC Its coding sequence has a use in the control of gene expression as a
XX CC promoter, coding sequence, 3'UTR or termination sequence, for controlling
XX CC the behaviour of a gene within the chromosome, as a tool for use in
XX CC genetic mapping, including a use in hybridisation assays, for recognition
XX CC or isolation of similar DNA fragments, or for the identification of a
XX CC particular organism
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XX OS Arabidopsis thaliana.
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/ PR	19-JUL-1999;	99US-0144335P.	/ PR	14-OCT-1999;	99US-0159323P.
/ PR	20-JUL-1999;	99US-0144352P.	/ PR	14-OCT-1999;	99US-0159330P.
/ PR	20-JUL-1999;	99US-0144632P.	/ PR	14-OCT-1999;	99US-0159331P.
/ PR	20-JUL-1999;	99US-0144884P.	/ PR	14-OCT-1999;	99US-0159637P.
/ PR	21-JUL-1999;	99US-0144814P.	/ PR	18-OCT-1999;	99US-0159584P.
/ PR	21-JUL-1999;	99US-0145088P.	/ PR	21-OCT-1999;	99US-0160741P.
/ PR	22-JUL-1999;	99US-0145085P.	/ PR	21-OCT-1999;	99US-0160787P.
/ PR	22-JUL-1999;	99US-0145087P.	/ PR	21-OCT-1999;	99US-0160788P.
/ PR	22-JUL-1999;	99US-0145089P.	/ PR	21-OCT-1999;	99US-0160770P.
/ PR	22-JUL-1999;	99US-0145099P.	/ PR	21-OCT-1999;	99US-0160814P.
/ PR	23-JUL-1999;	99US-0145145P.	/ PR	21-OCT-1999;	99US-0160815P.
/ PR	23-JUL-1999;	99US-0145218P.	/ PR	22-OCT-1999;	99US-0160980P.
/ PR	23-JUL-1999;	99US-0145224P.	/ PR	22-OCT-1999;	99US-0160981P.
/ PR	26-JUL-1999;	99US-0145276P.	/ PR	22-OCT-1999;	99US-0160989P.
/ PR	27-JUL-1999;	99US-0145913P.	/ PR	23-OCT-1999;	99US-0161404P.
/ PR	27-JUL-1999;	99US-0145918P.	/ PR	25-OCT-1999;	99US-0161405P.
/ PR	27-JUL-1999;	99US-0145919P.	/ PR	25-OCT-1999;	99US-0161406P.
/ PR	28-JUL-1999;	99US-0145951P.	/ PR	26-OCT-1999;	99US-0161359P.
/ PR	02-AUG-1999;	99US-0146386P.	/ PR	26-OCT-1999;	99US-0161360P.
/ PR	02-AUG-1999;	99US-0146388P.	/ PR	26-OCT-1999;	99US-0161361P.
/ PR	02-AUG-1999;	99US-0146389P.	/ PR	28-OCT-1999;	99US-0161930P.
/ PR	03-AUG-1999;	99US-0147038P.	/ PR	28-OCT-1999;	99US-0161932P.
/ PR	04-AUG-1999;	99US-0147204P.	/ PR	28-OCT-1999;	99US-0161993P.
/ PR	04-AUG-1999;	99US-0147302P.	/ PR	29-OCT-1999;	99US-0162142P.
/ PR	05-AUG-1999;	99US-0147192P.	/ PR	29-OCT-1999;	99US-0162143P.
/ PR	06-AUG-1999;	99US-0147260P.	/ PR	29-OCT-1999;	99US-0162238P.
/ PR	06-AUG-1999;	99US-0147303P.	/ PR	01-NOV-1999;	99US-0162891P.
/ PR	06-AUG-1999;	99US-0147416P.	/ PR	01-NOV-1999;	99US-0162894P.
/ PR	09-AUG-1999;	99US-0147493P.	/ PR	01-NOV-1999;	99US-0162855P.
/ PR	09-AUG-1999;	99US-0147935P.	/ PR	02-NOV-1999;	99US-0163091P.
/ PR	10-AUG-1999;	99US-0148171P.	/ PR	02-NOV-1999;	99US-0163092P.
/ PR	11-AUG-1999;	99US-0148319P.	/ PR	02-NOV-1999;	99US-0163093P.
/ PR	12-AUG-1999;	99US-0148341P.	/ PR	03-NOV-1999;	99US-0163248P.
/ PR	13-AUG-1999;	99US-0148565P.	/ PR	03-NOV-1999;	99US-0163249P.
/ PR	13-AUG-1999;	99US-0148684P.	/ PR	03-NOV-1999;	99US-0163281P.
/ PR	16-AUG-1999;	99US-0149369P.	/ PR	04-NOV-1999;	99US-0163379P.
/ PR	17-AUG-1999;	99US-0149175P.	/ PR	04-NOV-1999;	99US-0163380P.
/ PR	18-AUG-1999;	99US-0149426P.	/ PR	04-NOV-1999;	99US-0163381P.
/ PR	20-AUG-1999;	99US-0149722P.	/ PR	08-NOV-1999;	99US-0164146P.
/ PR			/ PR	08-NOV-1999;	99US-0164150P.

PR	08-NOV-1999	99US-0164511P
PR	09-NOV-1999	99US-0164259P
PR	09-NOV-1999	99US-0164260P
PR	10-NOV-1999	99US-0164317P
PR	10-NOV-1999	99US-0164318P
PR	10-NOV-1999	99US-0164319P
PR	10-NOV-1999	99US-0164321P
PR	10-NOV-1999	99US-0164544P
PR	10-NOV-1999	99US-0164545P
PR	10-NOV-1999	99US-0164548P
PR	12-NOV-1999	99US-0164870P
PR	12-NOV-1999	99US-0164871P
PR	12-NOV-1999	99US-0164959P
PR	12-NOV-1999	99US-0164960P
PR	12-NOV-1999	99US-0164961P
PR	12-NOV-1999	99US-0164962P
PR	15-NOV-1999	99US-0164926P
PR	15-NOV-1999	99US-0164927P
PR	15-NOV-1999	99US-0164929P
PR	16-NOV-1999	99US-0165661P
PR	16-NOV-1999	99US-0165669P
PR	16-NOV-1999	99US-0165671P
PR	17-NOV-1999	99US-0165911P
PR	17-NOV-1999	99US-0165918P
PR	17-NOV-1999	99US-0165919P
PR	18-NOV-1999	99US-0166157P
PR	18-NOV-1999	99US-0166158P
PR	18-NOV-1999	99US-0166173P
PR	19-NOV-1999	99US-0166411P
PR	19-NOV-1999	99US-0166412P
PR	22-NOV-1999	99US-0166641P
PR	22-NOV-1999	99US-0166733P
PR	22-NOV-1999	99US-0166750P
PR	23-NOV-1999	99US-0167362P
PR	24-NOV-1999	99US-0167233P
PR	24-NOV-1999	99US-0167234P
PR	24-NOV-1999	99US-0167235P
PR	24-NOV-1999	99US-0167382P
PR	30-NOV-1999	99US-0167902P
PR	30-NOV-1999	99US-0167904P
PR	30-NOV-1999	99US-0167908P
PR	01-DEC-1999	99US-0168231P
PR	01-DEC-1999	99US-0168232P
PR	01-DEC-1999	99US-0168233P
PR	02-DEC-1999	99US-0168546P
PR	02-DEC-1999	99US-0168548P
PR	02-DEC-1999	99US-0168549P
PR	03-DEC-1999	99US-0168673P
PR	03-DEC-1999	99US-0168674P
PR	07-DEC-1999	99US-0169278P
PR	07-DEC-1999	99US-0169298P
PR	07-DEC-1999	99US-0169302P
PR	08-DEC-1999	99US-0169491P
PR	08-DEC-1999	99US-0169492P
PR	16-DEC-1999	99US-0171098P
PR	16-DEC-1999	99US-0171107P
PR	16-DEC-1999	99US-0171114P
PR	19-JAN-2000	2000US-0176866P
PR	19-JAN-2000	2000US-0176867P
PR	19-JAN-2000	2000US-0176869P
PR	26-JAN-2000	2000US-0178466P
PR	27-JAN-2000	2000US-0178467P
PR	27-JAN-2000	2000US-0178545P
PR	27-JAN-2000	2000US-0178546P
PR	27-JAN-2000	2000US-0178547P
PR	28-JAN-2000	2000US-0178754P
PR	28-JAN-2000	2000US-0178755P
PR	01-FEB-2000	2000US-0179368P
PR	01-FEB-2000	2000US-0179395P
PR	03-FEB-2000	2000US-0180039P
PR	03-FEB-2000	2000US-0180139P

TOIG of: aag64458 check: 9499 from: 1 to: 542

ID AAG64458 standard; protein; 542 AA.

AC AAG64458

XX 22-OCT-2001 (first entry)

DT S. putrefaciens eicosapentanoic acid synthase enzyme 6.

DE Cyanobacterium; eicosapentanoic acid; EPA; plasmid.

XX Shewanella putrefaciens.

OS JP2001145490-A.

XX 29-MAY-2001.

XX 19-NOV-1999; 99JP-00329169.

XX 19-NOV-1999; 99JP-00329169.

XX (SAGA) SAGAMI CHEM RES CENT.

PA (BIOL-) BIOINDUSTRY KYOKAI SH.

PA (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIUTSU SOGO KEN.

XX WPI: 2001-406151/43.

DR N-PSDB; AAH47839.

XX A plasmid in which eicosapentanoic acid biosynthesis gene group is cloned and used to transform cyanobacterium so that it produces eicosapentanoic acid.

XX Claim 2; Page 60-61; 62pp; Japanese.

XX The invention relates to a plasmid prepared by cloning the Shewanella putrefaciens SCRC-2874 (FERM BP-1625) eicosapentanoic acid (EPA) synthesis gene cluster (AAH47833) into a broad host vector. The plasmid is used to transform cyanobacterium and produce EPA. The present sequence is that of a EPA biosynthesis enzyme of the invention

XX Sequence 542 AA;

AG64458 Length: 542 April 15, 2004 09:22 Type: P Check: 9499

MAPTATNMLSPNPAVTESN:SFDOVMEQIKDPFACVYVNHADHGFIAQTADIVTEQAA NSTDLP
VSAFTPALGTESLGDNFRVHGVKATYAGAWANGISEELIVIALGQAGILCSFGAGLIPSRVEAAIN
R:QALPNPGPYMNLHSPSEPALRGSEVELFLKHKVETVEASAFGLTPOIVYVRAAGLSRDQGVV
GNKVIAKSEIEVAEKFMMFAPAKMLQKLVDDSGTAEQMEALQVFNADDITAEADSGGHTNRPLVTL
LPTILALKEEIOAKYQYDTPIRVGGGVGTDDAALATFNMAAAYIVTGSINQACVAGASDHPRKLLAT
TEMADVTAAPADMFMGVKLVQVKGGLFPRANKLVEIVTRYDSIEAI PLDEREKLEKOVFPSSILDEI
WAGTVAHNERDPKQIERAEGNPKRMALIFRWVLGLSSRWNSGEGVREWDYQIWAGPALGAPNQWAKG
SYLDNYQDNADVDAKHLMYGAAYLNRLNSLTAQGVKVPQALLRWKPNQRMAL

TOIG of: aar30729 check: 500 from: 1 to: 870

ID AAR30729 standard; protein; 870 AA.

AC AAR30729

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1993 (first entry)

XX p100 protein from human herpes virus type 6.

XX antibody; monoclonal antibody; ELISA assays; CMV; cytomegalovirus.

XX Human herpesvirus 6.

XX EP524421-A1.

XX 27-JAN-1993.

XX 15-JUN-1992; 92EP-00110047.

XX 08-JUL-1991; 91EP-00111338.

XX (BEHW) BEHRINGWERKE AG.

XX Neipel F, Fleckenstein B;

XX WPI: 1993-028531/04.

XX P-PSDB; AAR30729.

XX Human herpes virus type 6 protein p100 DNA sequence - useful in prophylaxis, treatment and differential diagnosis of human herpes virus-6 infections.

XX Claim 1; Page 12; 25pp; English.

XX This sequence is the p100 protein from human herpes virus types 6. The protein and antibodies to it can be used for treatment or prevention of HHV-6 infections. The DNA, protein and Ab are also useful in eg. ELISA assays esp. for differentiating between HHV-6 and cytomegalovirus infections. These assays are more sensitive and specific than immunofluorescence methods currently used. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 870 AA;

AG30729 Length: 870 April 15, 2004 09:20 Type: P Check: 500

MDLORHPFPALWDRDKVERLTDFLSNLERDNDVLRHHPHTNSCVVRGDDVDDLKTLYNLLVLMY
HYVLSKRPDYNAWODITKLOSVNVEYLSKGLNKGI PENMTNKEKPESSQSDINELLLGNPTKQW
SNVADTYPVNLTAEDSSEIENQLQDAEKMLWTVYNINDPDWENGILTSINKLYIGKLFALATQSW
SKLEKVMSQIVITONHLSGHLRRHDFNIVSHRVLTQTLTGQVRFPUKITSDYDIKSSLESHSAS
KAFWSBEIGPNSLMDFPVLRGDIHNSLTPMSIDTKKSLDPAFLKSNRSLDGLRQWQPKFLELD
SYDNAGEXILLKEATLGCENYKATTPASSVLSMGSVSPSFTNLDLPLSSFTNLDRDKSHGNYK
IGPSGILDFNVKFFPNAQLNTNGVLLQDKTISGPSGGITDVVNGFANLHQNKNVSPWMSRTAAAN
ADFLDPVHPEOTGTPFLNNSDVAGSEAKHTTSTGTGVSFNVFLIKDLRGDGPFRKQSDIPKS
LTKENDKAIMHSEVTDGSDATEVYGAHNSPALRKIKOANDFFAGLNKKNDRDVLRGCKGNSKOLHSG
CNAKKEMSGKENDDKENTRNGQPSRLMDAARAGDEQYIQAGLQORVNLISQFTNLISLGEKIED
ILQNGRGTELKATENSGRESEANVEKLEVENQDMFNQLQNDLSVQSPFLPDPADLSREDSA
SPKDALDLKPGNGEREIDLAKKVKVGETSTDLKVGQDESFVPAQMKVETPEEKDDIIEQMVLRIQ
DGETDENTVSGPGVAESLDIEAKGESAIAS1

TOIG of: aar42456 check: 3609 from: 1 to: 543

ID AAR42456 standard; protein; 543 AA.

AC AAR42456;

XX

DT 25-MAR-2003 (revised)

DT 27-MAY-1994 (first entry)

XX

DE Enzyme involved in eicosapentaenoic acid (EPA) synthesis.

XX

KW EPA; eicosapentaenoic acid synthetase; drug; anticoagulant; hypolipemic; hypoglycemic; antihypertensive; anticancer; pesticide; foodstuff; additive.

XX

OS Shewanella putrefaciens.

XX

PN WO9323545-A1.

XX

PD 25-NOV-1993.

XX

PF 14-MAY-1993; 93WO-JP000641.

XX

PR 15-MAY-1992; 92JP-00147945.

XX

PA (SAGA) SAGAMI CHEM RES CENTRE.

XX

PI Yazawa K, Yamada A, Kato S, Kondo K;

XX

DR WPI; 1993-386577/48.

DR N-PSDB; AAQ51128.

XX

PT Gene coding for eicosapentaenoic acid synthetase - is isolated from Pseudomonas, Alteromonas or Shewanella and used for recombinant prodn. of eicosapentaenoic acid.

XX

PS Claim 10; Page 91-94; 106pp; Japanese.

XX

CC EPA is useful as a drug, having anticoagulant, hypolipemic, hypoglycemic, antihypertensive and anticancer activity. It is also a pesticide and is useful as a nutritional foodstuff and animal feed additive. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 543 AA;

AA42456 Length: 543 April 15, 2004 09:20 Type: P Check: 3609 ..

aa42456

MNPTATNEMLSPPWPWAVTESNISFDVQVMEQQLKDFSRACYYVNHADHGFIAQTADIVTEQANSTDLF
 VSAFTPALGTESLGDNNFRVHGVKYAYAGAMANGISSEELVIALQAGILCGSFGAAGLIPSRVERAI
 NRIQALPNGPYMFLNHSPEALERSGVELFLKHVRTVEASAFGLTPOIVYRAAGLSRDAQGVV
 VGNKVIKVSRTVEAKFMPAPAKMLQKLVDDGSIATQEMELAQVPMADITAEADSGGHTDNRPLVT
 LLPTILALKEEIQAKYQYDTPIRVCGGSGVGTDDAALATFNGAAYIVTGSINQACVEAGSDHTRKLLA
 ITTQADVTPAAPADMFMGVKLVQVKGTLFPFRANKLYEITRYDYSIEALPLDEREKLEKQVFRSSLDE
 IWAGTVAHFNERDPKQIERAEGNPKRQVALIFRWYGLSSRWSNBSGVEGMDYQIWAGPALGAFNQWAK
 GSYLDNYQDRNAVDLAKHLYGAAYLNRLNSLTAAQGVKVPQAQLLRWKNQRMAL

TOIG of: aar99465 check: 3609 from: 1 to: 543

ID AAR99465 standard; protein; 543 AA.

AC AAR99465;

XX

DT 30-JAN-1997 (first entry)

XX

DE Biosynthetic enzyme of icosapentaenoic acid synthase.

XX

KW Icosapentaenoic acid synthase; EPA; drugs; agrochemicals; foodstuffs; animal feed; lipid balance correction; antihypertensive; antiinflammatory; anticancer agent.

XX

OS Shewanella putrefaciens.

XX

PN WO9621735-A1.

XX

PD 18-JUL-1996.

XX

PF 12-JAN-1996; 96WO-JP000030.

XX

PR 13-JAN-1995; 95JP-00004299.

XX

PA (SAGA) SAGAMI CHEM RES CENTRE.

XX

PI Yazawa K, Yamada A, Kondo K;

XX

DR WPI; 1996-342288/34.

DR N-PSDB; AAT34137.

XX

PT Production of icosapentaenoic acid using transformed E. coli - uses DNA coding for icosapentaenoic acid synthase derived from Shewanella strain.

XX

PS Claim 7; Page 128-131; 145pp; English.

XX

CC The DNA sequence (AAT34137) which encodes the biosynthetic enzymes of icosapentaenoic acid (EPA) can be used to transform Escherichia coli. The DNA sequence allows efficient microbial production of EPA, which is a raw material for drugs, agrochemicals, foods and animal feedstuffs. EPA is also useful for lipid balance correction and as an antihypertensive, antiinflammatory and anticancer agent

XX

SQ Sequence 543 AA;

AA99465 Length: 543 April 15, 2004 09:20 Type: P Check: 3609 ..

aa99465

MNPTATNEMLSPPWPWAVTESNISFDVQVMEQQLKDFSRACYYVNHADHGFIAQTADIVTEQANSTDLF
 VSAFTPALGTESLGDNNFRVHGVKYAYAGAMANGISSEELVIALQAGILCGSFGAAGLIPSRVERAI
 NRIQALPNGPYMFLNHSPEALERSGVELFLKHVRTVEASAFGLTPOIVYRAAGLSRDAQGVV
 VGNKVIKVSRTVEAKFMPAPAKMLQKLVDDGSIATQEMELAQVPMADITAEADSGGHTDNRPLVT
 LLPTILALKEEIQAKYQYDTPIRVCGGSGVGTDDAALATFNGAAYIVTGSINQACVEAGSDHTRKLLA
 ITTQADVTPAAPADMFMGVKLVQVKGTLFPFRANKLYEITRYDYSIEALPLDEREKLEKQVFRSSLDE
 IWAGTVAHFNERDPKQIERAEGNPKRQVALIFRWYGLSSRWSNBSGVEGMDYQIWAGPALGAFNQWAK
 GSYLDNYQDRNAVDLAKHLYGAAYLNRLNSLTAAQGVKVPQAQLLRWKNQRMAL

TOIG of: aaU5346 check: 8069 from: 1 to: 79

ID AAU5346 standard; protein; 79 AA.

AC AAU5346

XX

XX

DT 27-FEB-2002 (first entry)

XX

DE Propionibacterium acnes immunogenic protein #26242.

XX

XX

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.

XX

OS Propionibacterium acnes.

XX

XX

PN WO200181581-A2.

XX

XX

PD 01-NOV-2001.

XX

XX

PF 20-APR-2001; 2001WO-US012865.

XX

XX

PR 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX

XX

PA (CORI-) CORIXA CORP.

XX

XX

PI Steiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX

XX

DR N-PSDB; AAS59666.

DR

XX

XX

PT Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX

XX

PS Example 1; SEQ ID NO 26541; 1069pp; English.

XX

XX

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

CC polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by

CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for

CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

XX

SQ Sequence 79 AA;

AAU5346 Length: 79 April 15, 2004 09:23 Type: P Check: 8069

aaU5346

TIIVSGVVMARAPNATFCRSPVIRPAPKESPPKRSRLGRSTERTKPVSFDAIAD

QSLRLAVRTI

TOIG of: aaU6759 check: 99 from: 1 to: 113

ID AAU6759 standard; protein; 113 AA.

AC AAU6759

XX

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DT 13-FEB-2002 (first entry)

XX

DE Propionibacterium acnes immunogenic protein #27655.

XX

XX

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.

XX

OS Propionibacterium acnes.

XX

XX

PN WO200181581-A2.

XX

XX

PD 01-NOV-2001.

XX

XX

PF 20-APR-2001; 2001WO-US012865.

XX

XX

PR 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX

XX

PA (CORI-) CORIXA CORP.

XX

XX

PI Steiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX

XX

DR N-PSDB; AAS59754.

DR

XX

XX

PT Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX

XX

PS Example 1; SEQ ID NO 27954; 1069pp; English.

XX

XX

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

CC polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by

CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for

CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

XX

SQ Sequence 113 AA;

AAU6759 Length: 113 April 15, 2004 09:24 Type: P Check: 99

aaU6759

PETANGSFCGSGQORFTRADPPAANDSTQORVTIEVSGVVMARAPNATFCRSPVIRPATRP

AAKSPPTKRSRLGRSTERTKPVSFDAIADQSLAVRTI

TOIG of: aaw37053 check: 3609 from: 1 to: 543

ID AAW37053 standard; protein; 543 AA.
 AC AAW37053
 DT 03-JUL-1998 (first entry)
 DE S. putrefaciens EPO biosynthesis gene cluster ORF9 product.
 KW SCRC-2874; FERM BP-1625; eicosapentaenoic acid; EPA;
 biosynthesis gene cluster; synthetase.
 OS Shewanella putrefaciens.
 PN WO9801565-A1.
 PD 15-JAN-1998.
 PF 09-JUL-1997; 97WO-JP002371.
 PR 10-JUL-1996; 96JP-00180845.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PI Yazawa K, Yamada A, Kondo K, Kato S;
 WPI; 1998-101060/09.
 DR N-PSDB; AAW0503.
 PT Eicosapentaenoic acid produced by culture of transformed *Escherichia coli*
 containing an eicosapentaenoic acid synthetase gene derived from the
 marine microorganism *Shewanella*.
 PS Example 1; Page 93-97; 110pp; Japanese.
 CC The present sequence is encoded by the *Shewanella putrefaciens* SCRC-2874
 (FERM BP-1625) eicosapentaenoic acid (EPA) biosynthesis gene cluster. A
 novel EPA (useful in drugs, pesticides, foods and feedstuffs) is encoded
 by synthetase enzyme gene sequences comprising parts of the full sequence
 of the synthetase gene from the marine microorganism *S. putrefaciens* SCRC
 -2874 (FERM BP-1625), in which at least 1 of the 9 open reading frames
 (ORF) (numbered 2-10) in the gene have been deleted. In particular the
 gene sequences comprising the following parts of the full gene: (1) bases
 8081-9441, 12314-13084 and 13889-32520; (2) bases 8081-9441, 12314-13084,
 13889-32520 and 34627-35559; (3) bases 8081-9441, 12314-13084 and 13889-
 35559; (4) bases 8081-9441, 9681-13084 and 13889-32520; (5) bases 8081-
 9441, 9681-13084, 13889-32520 and 34627-35564; and (6) bases 8081-9441,
 9681-13084 and 13889-35564, are claimed

Sequence 543 AA;

AAW37053 Length: 543 April 15, 2004 09:21 Type: P Check: 3609 ..
 AAW37053
 MNPTATNEMLSPPWPVAVTESNIFSDVQVMEQOLKDFSRACYVNVNADHGFAGIAQTADIVTEQANSTDLPL
 VSAFTPALGTSELGNNFRVGHVKYAYAGAMANGISSEELVIALQAGILCGSFGAAGLTPSRVERAAI
 NRIQAALPNGPYMFNLIHSPSEPALERSVELFLKHKVTVEASAFGLTQIIVYRAAGLSRDAQGVV
 VGNKVIKTSRTEVAFKFWMPAPAKMLQKLVDDGSIATQAEQMLQVPMADDITAEADSGGHTNRPVLT
 LLPTILALKEIEIOAKYQYDTPIRVCGCGGVTGPDALATFNMGAAIVITGSIINQACVEAGADSDHTRKLLA
 TTEWADVTFAPADMFEMGVKLVQVKGTLFPNRAKLEIYTRYDSIEAFLDREKLEKQVFPSSLLDE
 IWAGTVAFNERDPQIERAEGNPKRKVALIFRWYLGLSRWSNGEVGEMDYQIOWAGPALGAFNQWAK
 GSYLDNYQDRNAVLDLAKELMVAAYLNRINSLTAQGVKVPAPQLLRNKPQRMA1

TOIG of: aaw89403 check: 3609 from: 1 to: 543

ID AAW89403 standard; protein; 543 AA.
 AC AAW89403
 DT 19-OCT-1999 (first entry)
 DE S. putrefaciens PKS-like cluster ORF 9 protein.
 KW Polyketide-like synthesis; PKS; PKS-like gene; PUFA; EPA; transgenic;
 poly-unsaturated fatty acid; eicosapentaenoic acid; docosahexanoic acid;
 EPA; oil; dietary supplement; infant feeding formulation; malnutrition;
 intravenous feeding formulation; cooking oil; fat; anti-inflammatory;
 cholesterol; open reading frame; ORF.
 PN Shewanella putrefaciens.
 PD WO9855625-A1.
 PF 10-DEC-1998.
 PR 04-JUN-1999; 98WO-US011639.
 PA 04-JUN-1997; 97US-0048650P.
 PI (CALJ) CALGENE LLC.
 PI Pacciotti D, Metz JG, Lassner M;
 WPI; 1999-070271/06.
 DR N-PSDB; AAZ00331.
 PT New nucleic acid encoding polyketide-like synthesis enzymes of *Vibrio*
 marinus - and transformed plants and microbes that produce
 polyunsaturated fatty acids, useful as pharmaceuticals and food
 supplements.
 CC Claim 17; Fig 4; 153pp; English.
 CC The invention provides polyketide-like synthesis (PKS)-like genes that
 are used for the production of long chain polyunsaturated fatty acid
 (PUFA) productions. Genes responsible for eicosapentaenoic acid (EPA)
 production in *Shewanella putrefaciens* and novel genes associated with the
 production of docosahexanoic acid (DHA) in *Vibrio marinus* are used to
 generate transgenic plants that can express transgenes encoding PKS-like
 genes associated with PUFA production. The PKS-like genes are used to
 transform plants and microbial cells to give recombinants having altered
 contents of PUFA (specifically DHA and EPA). Oils from these plants are
 useful as dietary supplements (in infant feeding formulations, to give a
 PUFA profile closer to that of human milk; for treating malnutrition; in
 intravenous feeding formulations; in cooking oils, fats etc.), also as
 anti-inflammatory agents and for reducing cholesterol levels. Fragments
 from the genes are useful as probes to isolate related molecules or to
 detect organisms that express PKS-like genes. The method facilitates
 large scale production of PUFA by providing new pathways for their
 synthesis or suppressing interfering pathways. Expression of PUFA in
 seeds allows simple recovery, as oil which can be engineered to have a
 particular PUFA profile. Expression in microbes also allows simple
 recovery and control of PUFA profile and is not subject to external
 variables such as weather or food supply. Sequences AAW89396-404
 represent different ORF proteins of *S. putrefaciens* PKS-like cluster
 Sequence 543 AA;

AAW89403 Length: 543 April 15, 2004 09:21 Type: P Check: 3609 ..
 AAW89403
 MNPTATNEMLSPPWPVAVTESNIFSDVQVMEQOLKDFSRACYVNVNADHGFAGIAQTADIVTEQANSTDLPL
 VSAFTPALGTSELGNNFRVGHVKYAYAGAMANGISSEELVIALQAGILCGSFGAAGLTPSRVERAAI
 NRIQAALPNGPYMFNLIHSPSEPALERSVELFLKHKVTVEASAFGLTQIIVYRAAGLSRDAQGVV
 VGNKVIKTSRTEVAFKFWMPAPAKMLQKLVDDGSIATQAEQMLQVPMADDITAEADSGGHTNRPVLT
 LLPTILALKEIEIOAKYQYDTPIRVCGCGGVTGPDALATFNMGAAIVITGSIINQACVEAGADSDHTRKLLA

TTWADVWMAADMEFGVKLVKRGTLFPMRANKLYEITRYDSIEATPLDEREKLEKQVFRSSIDE
IWAGTVAHNERDFKQIERAENGFKRMALIFRWYLGSSRWNSGVEGRENDEYQIWAGPALGAFNQWAK
GSYLDNYQDRNAVLDLAKHLLMYGAAYLNRINSUTAQGVKVPFQALLRWKPNQMA1

TOIG of: abm61865 check: 8069 from: 1 to: 79
ABM61865 standard; protein; 79 AA.

ABM61865;

20-OCT-2003 (first entry)

Propionibacterium acnes predicted ORF-encoded polypeptide #26541.

Acne vulgaris; antiseborrheic; dermatological; antibacterial;
immunostimulant; immune response; vaccine.

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825.

(CORI-) CORIXA CORP.

Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
Barth B, Vallieue-Douglas J;

WPI; 2003-391789/36.

N-PSDB; ACF64595.

New Propionibacterium acnes polypeptides and polynucleotides encoding the
polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
or for stimulating an immune response specific for a P. acnes protein.

Example 1; SEQ ID NO 26541; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
encoding a Propionibacterium acnes protein. The invention also relates to
polypeptides encoded by the polynucleotides (ABM35524-ABM64536) and to
immunogenic fragments of P. acnes polypeptides. The invention
additionally encompasses expression vectors and host cells comprising a
polynucleotide of the invention; antibodies against polypeptides of the
invention; fusion proteins comprising a polypeptide of the invention; a
method for stimulating an immune response specific for a P. acnes
polypeptide and an isolated T cell population comprising P. acnes polypeptides,
via this method; a vaccine composition (comprising P. acnes polypeptides,
polynucleotides, antibodies, fusion proteins, T cell populations, or
antigen-presenting cells that express the polypeptide); a method and kit
for detecting or determining the presence or absence of P. acnes in a
patient; and a method for inhibiting the development of P. acnes in a
patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
proteins, T cell populations or antigen-presenting cells that express the
polypeptides are useful for diagnosing, preventing or treating acne
vulgaris, or for stimulating an immune response specific for a P. acnes
protein. The polynucleotides can also be used as probes or primers for
nucleic acid hybridisation. The vaccine composition is useful for the
stimulation of an immune response against P. acnes, or for treating acne,
and the kit is useful for performing a diagnostic assay. The present
sequence represents a polypeptide predicted to be encoded by an ORF (open
reading frame) contained within the P. acnes polynucleotides of the
invention. Note: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 79 AA;

ABM61865 Length: 79 April 15, 2004 09:24 Type: P Check: 8069 ..

abm61865

TIEVSGVVMARAPWAAPNSTAFCSVPSVIRPATRPAAKEGPPPTRRSSISRLGRSTERTKVFSDHAID
QSLRLAVRTI

TOIG of: abm63278 check: 99 from: 1 to: 113

ID ABM63278 standard; protein; 113 AA.

XX ABM63278

AC

XX

DT 20-OCT-2003 (first entry)

XX

DE Propionibacterium acnes predicted ORF-encoded polypeptide #27954.

XX

KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.

XX

OS Propionibacterium acnes.

XX

PN WO2003033515-A1.

XX

PD 24-APR-2003.

XX

PF 11-OCT-2002; 2002WO-US032727.

XX

PR 15-OCT-2001; 2001US-00978825.

XX

PA (CORI-) CORIYA CORP.

XX

PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL; Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D; Barth B, Valliee-Douglas J;

PI

XX

DR WPI; 2003-381789/36.

DR N-ESDB; ACF64683.

XX

PT

PT

PT

XX

PS Example 1; SEQ ID NO 27954; 1481pp; English.

XX

CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising P. acnes polypeptides, via this method; a vaccine composition (comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide), a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (Open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 113 AA;

ABM63278 Length: 113 April 15, 2004 09:24 Type: P Check: 99 ..

abm63278

PERTANGSPCHSGSDORFTADPPAANDSTSRVIEVSPGVVMAEPAWAPNSAFCRSPVSIAPTRP

AAK66PPTTSRLRGRSTERTKPVSPDHAIADQSLRAVT1

! FINDPATTERNS on pir.* allowing 0 mismatches

! 1 E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R,I) (T,S,N)R

1 XPEB12 ck: 1901 len: 871 ! major antigenic structural protein p100 - h
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R
E(S) (Q) (F) (S) (D) (I) (N)R(A)

121: NKEKF ESQFSDINRA LIRIG

1 D97264 ck: 8698 len: 497 ! galactose-1-phosphate uridylyltransferase [im
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R
E(H) (I) (P) (M) (K) (I) (S)R(I)

226: IILNN EHIPKISRI TFENL

1 T30186 ck: 3609 len: 543 ! hypothetical protein 8 - Shewanella sp.
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R
E(Q) (Q) (L) (K) (D) (F) (S)R(A)

30: DVQVM EQQLKDFSA CYVN

1 B90396 ck: 6793 len: 220 ! hypothetical protein SSO2259 [imported] - S
E(Q,S,H,Y,E) (S,Q,I,T,N,P) (F,T,S,P,L,I) (N,S,K,M,T,P) (D,K,T,E) (F,L,R
E(E) (I) (I) (N) (D) (L) (S)R(I)

137: LINHW BEINDLSRI DLTNE

Databases searched:

NBRF, Release 78.0, Released on 24Nov2003, Formatted on 25Nov2003

Total finds: 4
Total length: 96,191,526
Total sequences: 283,566
CPU time: 02:57.60

TOIG of: b90396- check: 6793 from: 1 to: 220
P1/B90396- hypothetical protein SSO2259 [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C/Accession: B90396
R.; She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez,
M.J.; Chan-Waiher, C.C.Y.; Clausen, I.G.; Curtis, B.A.; De Moers, A.; Etrauso,
G.; Fletcher, C.; Gordon, P.M.K.; Heikamp-de Jong, I.; Jeffries, A.C.; Kozera,
C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; Schenk, M.E.;
Theriault, C.; Tolstrup, N.; Charlebois, R.L.; Doolittle, W.F.; Duguet, M.;
Gaasterland, T.; Garrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.;
submitted to Genbank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: B90396
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-220 <KUR>
A/Cross-references: GB:AE006641; NID:g13815561; PIDN:AAK42425.1; GSPDB:GN00155
C/Genetics:
A/Gene: SSO2259
B90396 Length: 220 April 15, 2004 09:27 Type: P Check: 6793 ..
MTNGEVALDNLLKDEKLSLNKILVINTDRLGILDVKGILEEDNTGKIGSLTSDVLELVNWD
KVIKTKLFNEDNIYNIQFLINLIDKVRSGKILDPILGLEDSESGKIINALINDFTLNLNWEHII
ADPSRDLTNFKYITLLVSAIGALKTENVKPITTSIWEYKLLKDPDIQRGUGVAASVLKRGIDYVDPK
GLAFAVEVEKKLI

TOIG of: d97264 check: 8688 from: 1 to: 497
P1/D97264- galactose-1-phosphate uridylyltransferase [imported] - Clostridium
acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 27-Oct-2003
C/Accession: D97264
R.; Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson,
R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.;
Sabatie, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.;
Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing
Bacterium Clostridium acetobutylicum.
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: D97264
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-497 <KUR>
A/Cross-references: GB:AE001437; PIDN:AAK80903.1; PID:g15026015; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC2961
C/Superfamily: galactose-1-phosphate uridylyltransferase, Bacillus type
D97264 Length: 497 April 15, 2004 09:26 Type: P Check: 8688 ..
MINHEINKLLAFSLKGLIQEDDKIYSSNMLAGFLNLDNFYEETSDVPSTATALNQLLAYAVKENLIN
DTVAERDLFTDKMNCMPRPSEVINNFNLNNSPKETASYVKLSIASNYIKRDKIDKNTWKPTPEY
GDLDITINLSKPKDPRDTAKAKLSKTSYKCLCKENEGFVGNINHPAQTLRIIPLELNKSKWFLOY
SPYTYNEHCILLNNEHTIPMKTSRSTFENLISFDILPHYFAGSNADLPYGGSTLSHDHYGGGYTFAM
EKAPVEKYSIKGYEDI SVGRVYKWPMSVIRSSKNKTKLINLAHILTSWRYNSDKTQCSILSHTSSEPHN
TITPIARKKNEYELDLVLNRNRTDENTPLGTFPHNEVHHIKENIGLIEVMGLAVLPARKSELALIK
ENLIEKKKDISNDSTISIKHTWYKYLIDNYKNISSENDICILKKEVGITKFLVILKAGVFKRNSSGUSAF
DKFINIL1

TOIG of: t30186 check: 3609 from: 1 to: 543
; P1: T30186 - hypothetical protein 8 - Shewanella sp.
; C: Species: Shewanella sp.
; C: Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
; C: Accession: T30186
; R: Takeyama, H.; Takeda, D.; Yazawa, K.; Yamada, A.; Matsunaga, T.
; Microbiology 143, 2725-2731, 1997
; A: Title: Expression of the eicosapentaenoic acid synthesis gene cluster from
; Shewanella sp. in a transgenic marine cyanobacterium, Synechococcus sp.
; A: Reference number: 220764; MUID: 97419510; PMID: 9274025
; A: Accession: T30186
; A: Status: preliminary; translated from GB/EMBL/DBJ
; A: Molecule type: DNA
; A: Residues: 1-543 <TAK>
; A: Cross-references: EMBL:U73935; NID:G2529413; PID:G2529421; PIDN:AA881126.1
; A: Experimental source: strain SCRC-2738
; T30186 Length: 543 April 15, 2004 09:26 Type: P Check: 3609 ..
; NNPATNEMLSPPWAVTESISFDVQVMSQQLKQDPSRCYVNVNADHGFAGIACTADIVTEQAANSTDLIP
; VSAFTPALGTESLGDNFRVHGVKYAYAGAWANGISSSELVIALGQGLCGSFGAAGLIPSRVEAAI
; NRIQAALPNQPMFNLIHSPALERSGVLEFLKHKTVEASAFGLTPQIVYRAGLRDQAGKVV
; VGNKVIARVTEVAEFMMPAPAKMLQKLVDDGSITAEQMEALQVPMADITAEADSGHTDNRPLVT
; LLPITLAKSEIOAKYOYDPIRVGCGGVGTPDAALATFNMGAAVIVTGSINQACVEAGSDHTRKLLA
; TTEWADVMTAPADMFMGVKLOVKGGLPPNRANKLVELVTEVDSIEAIPIDEREKLEKQVFRSSLDE
; IWAGTVAFNERDPKQIERAEGNPKRMALIPRYLGLSRWNSGEVGRNDYQIHWAGFALGAFNQWAK
; GSYLDNYQDRNAVNDLAKHLYGAAYLNRLNSLTAAQGVKVPFAQLLRWKNQORVAI

TOIG of: xpbel2 check: 1901 from: 1 to: 871
; P1: XBBE12 - major antigenic structural protein p100 - human herpesvirus 6
; (strain UI102)
; C: Species: human herpesvirus 6
; C: Date: 30-Jun-1993 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
; C: Accession: T09303; A42533
; R: Nicholas, J.; Martin, M.
; J. Virol. 68, 597-610, 1994
; A: Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
; genome of human herpesvirus 6 encoding human cytomegalovirus immediate-early
; gene homologs and transactivating functions.
; A: Reference number: Z16644; MUID: 94118404; PMID: 8289364
; A: Accession: T09303
; A: Status: preliminary; translated from GB/EMBL/DBJ
; A: Molecule type: DNA
; A: Residues: 1-871 <NIC>
; A: Cross-references: EMBL:L25528; NID:G451932; PIDN:AAA16716.1; PID:G451934
; R: Naipel, F.; Ellinger, K.; Fleckenstein, B.
; J. Virol. 66, 3918-3924, 1992
; A: Title: Gene for the major antigenic structural protein (p100) of human
; herpesvirus 6.
; A: Reference number: A42533; MUID: 92260671; PMID: 1374813
; A: Accession: A42533
; A: Molecule type: DNA
; A: Residues: 2-871 <NEI>
; A: Cross-references: GB:M87287; NID:G330673; PIDN:AAA46012.1; PID:G330674
; C: Genetics:
; A: Gene: P1F1
; C: Superfamily: human herpesvirus large structural phosphoprotein; large
; structural phosphoprotein homology
; C: Keywords: phosphoprotein
; F: 7-368/Domain: large structural phosphoprotein homology <CLS>
; XBBE12 Length: 871 April 15, 2004 09:26 Type: P Check: 1901 ..
; xpbel2
; NMDLQRHPIPFAMLDKRDVKVERLTDFLSNLERLDNVLDREHPHTVNSCVVREGDDVDLKLTLNLIWLM
; YHYVLSKRPPDYNAIWQDITKLQSVVYNSKGLNKGIFNMFTNKEKFSQSDINRALRLGNFIKW
; GSNVAIDTPYNLTAEDSSEIENNLQDAENIYVTVNINPDWENGYLITSINKLYLGLFLALTSQ
; WSKLEKVMASQIVITONHLSCHLRSDNENIYVSHVLQTLTGQVSEFLKILTSYDIIKSSLES
; SKAFSMEIGPSNLMDFVPLRGDIHSLNLTLPMSIDITKSSLDPAKLKSNRSLDSFLMRQRPKFL
; DSDVNAKEKILLKEATLGGENVKATTPASSVLSMGSVSPSSFTSNLPLSSFTSNLDRKSHGNY
; KIGPSGILDFNVKPPNAQNTNGDILQDKTSIGSPSSGITVYVNGFANLHONKSNVSPPSRNTAA
; NADFLDFVHRFVEQTPFVLNNSDVAGSEAKHTTSTETGVSPRVNVLKDLRGKDGFRKQSDIPK
; SLTKERNDAIMHSREVTGDSGDATETVGARNSPALRKIKOANDPFAGLNKKNRDVLRGKGNKDLHS
; GGNAKKMGSKFNDKEMTRNGQSPSLMGDARNAGDEQVIOAGLQGVNLLSQFTNLSIGEGIE
; DILONQRGTLEKLA TENKSGRESEANVEKLLVSNPQDMKFNRLQNDLDSVQSPFLPADLSRELD
; ASFKDALDLKLPNGRERIDLALEKRVGETETSDLKVQDESFPVPAQIMKVFEEKDDIEQKVLIR
; QDGETDENTVSGPGVAESLDIEAKGESAIAS1

! FINDPATTERNS on swp:* allowing 0 mismatches

1 1 E(Q,S,H,Y,E)(S,Q,I,T,N,P)(F,T,S,P,L,I)(N,S,K,M,T,P)(D,K,T,E)(F,L,R,I)(T,S,N,R)

1 1 GALT_CLOAB ck: 8688 len: 497 1 Q97ez4 clostridium acetobutylicum. galactos

E(Q,S,H,Y,E)(S,Q,I,T,N,P)(F,T,S,P,L,I)(N,S,K,M,T,P)(D,K,T,E)(F,L,R
E(H)(I)(P)(M)(K)(I)(S)(R(I)
226: IILNN EHIPKISRI TFENL

1 1 PI00_HSV60 ck: 500 len: 870 1 Q00701 human herpesvirus (type 6 / strain u

E(Q,S,H,Y,E)(S,Q,I,T,N,P)(F,T,S,P,L,I)(N,S,K,M,T,P)(D,K,T,E)(F,L,R
E(S)(Q)(F)(I)(N)(R(A)
120: NKEKF ESQFSINRA LLRLG

1 1 PFDA_METKA ck: 9337 len: 157 1 Q8tuy7 methanopyrus kandleri. prefoldin alp

E(Q,S,H,Y,E)(S,Q,I,T,N,P)(F,T,S,P,L,I)(N,S,K,M,T,P)(D,K,T,E)(F,L,R
E(S)(I)(I)(S)(E)(L)(N)(R(V)
39: QIDLI ESSISELNRV EETLK

1 1 Q33907 ck: 3609 len: 543 1 Q33907 shewanella sp. scrc-2738. hypothetic

E(Q,S,H,Y,E)(S,Q,I,T,N,P)(F,T,S,P,L,I)(N,S,K,M,T,P)(D,K,T,E)(F,L,R
E(Q)(Q)(L)(K)(F)(S)(R(A)
30: DVQVM EQQLKDFSA CIVVN

1 1 Q9ESP3 ck: 4988 len: 1,851 1 Q9esp3 rattus norvegicus (rat). mucin (frag

E(Q,S,H,Y,E)(S,Q,I,T,N,P)(F,T,S,P,L,I)(N,S,K,M,T,P)(D,K,T,E)(F,L,R
E(S)(N)(S)(T)(L)(S)(R(V)
130: LRRGL ESNSTLSRV IMKLD

1 1 Q80Z21 ck: 6085 len: 1,726 1 Q80z21 mus musculus (mouse). secreted gel-f

E(Q,S,H,Y,E)(S,Q,I,T,N,P)(F,T,S,P,L,I)(N,S,K,M,T,P)(D,K,T,E)(F,L,R
E(S)(N)(T)(T)(L)(S)(R(V)
126: LRRVQ ESNSTLSRV TMKLD

1 1 Q97WG2 ck: 6793 len: 220 1 Q97wg2 sulfolobus solfataricus. hypothetica

E(Q,S,H,Y,E)(S,Q,I,T,N,P)(F,T,S,P,L,I)(N,S,K,M,T,P)(D,K,T,E)(F,L,R
E(E)(I)(I)(N)(D)(L)(S)(R(I)
137: LINHW EEIINDLSRI DLTNP

Databases searched:

SWISS-PROT, Release 42.7, Released on 15Dec2003, Formatted on 15Dec2003

SEXPRES, Release 25.0, Released on 17Oct2003, Formatted on 18Oct2003

Total finds: 7

Total length: 367,588,357

Total sequences: 1,158,722

CPU time: 12:01.74

TOIG of: galt_cloab check: 8688 from: 1 to: 497

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; ID GALT_CLOAB STANDARD; PRT; 497 AA.
; AC Q97E24;
; DT 28-FEB-2003 (Rel. 41, Created)
; DT 28-FEB-2003 (Rel. 41, Last sequence update)
; DT 10-OCT-2003 (Rel. 42, Last annotation update)
; DE Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12) (Gal-1-P
; DE uridylyltransferase) (UDP-glucose--hexose-1-phosphate
; DE uridylyltransferase).
; DE GALT OR CAC2961.
; GN Clostridium acetobutylicum.
; OS Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
; OC Clostridium.
; OC NCBI_TaxID=1488;
; OX [1]
; RN RP
; RP SEQUENCE FROM N.A.
; RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
; RX MEDLINE=21393345; PubMed=11466286;
; RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
; RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
; RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
; RA Bennett G.N., Koonin E.V., Smith D.R.;
; RA "Genome sequence and comparative analysis of the solvent-producing
; RA bacterium Clostridium acetobutylicum.";
; RL J. Bacteriol. 183:4823-4838(2001).
; CC -1- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose 1-phosphate =
; CC alpha-D-glucose 1-phosphate + UDP-galactose.
; CC -1- PATHWAY: Galactose metabolism; second step.
; CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
; CC -1- SIMILARITY: Belongs to the galactose-1-phosphate
; CC uridylyltransferase family 2.
; CC
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; CC
; CC EMBL; AE007793; AAK80903.1; -.
; CC PIR; D97264; D97264.
; CC HAMAP; MF 00571; -.
; CC InterPro; IPR000766; GalP_transf_II.
; CC InterPro; IPR005850; GalP_Utransf_C.
; CC InterPro; IPR005849; GalP_Utransf_N.
; CC InterPro; IPR005934; GalP2.
; CC Pfam; PF02744; GalP_UDP_tr_C; 1.
; CC TIGRfam; TIGR01239; galT_2; 1.
; CC PROSITE; PS01163; GAL_P_UDP_TRANSF_II; 1.
; CC Transferase; Nucleotidyltransferase; Galactose metabolism;
; CC Complete proteome.
; CC SEQUENCE 497 AA; 5728 MW; 81B9D089CDA9F5CC CRC64;

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GALT_CLOAB Length: 497 April 15, 2004 09:30 Type: P Check: 8688

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; GALT_CLOAB
; MINHEINKILLASLKGLOEDDKIVSSNMAGLNLNVEFEELSDVPSTATAILLQLLAYAKENLIN
; DVAERDLFTKIMCQMPRESEVNNRNLNPKKATSYKLSIASNYIRDRIDKNITWKTET
; GDDITINUSKEKQPRDAPKLSKSTSPKCLCKNEGYNINHPARQTLRIIPLELNKSKWFLQY
; SPYTYNEHCIIINNEHPKMSKSTFNLISFDILPHYAGSNADLPYVGGSLSDHVGQGRYTFAM
; EKAPVEKEYSIKGYEISVGRYKMPMSVIRISKNKTKLINAEHLISWENYSDKQSLSHSGSEPHN
; TITPARKNEVEYELDLVLRNKRNTENPLGTFPHNEVHHIKKENIGLIEWMGLAVLPARKSELALIK
; ENLIEKKDISNDSTISKINTYKVIILDNKYNI SEENIDCILKKEVGKFEVLVKGHPKRNSSGLSF
; DFEINILL

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; TOIG of: p100_hsv6u check: 500 from: 1 to: 870
; ID P100_HSV6U STANDARD; PRT; 870 AA.
; AC Q00701;
; DT 01-APR-1993 (Rel. 25, Created)
; DT 01-APR-1993 (Rel. 25, Last sequence update)
; DT 15-OCT-2001 (Rel. 40, Last annotation update)
; DE Large structural phosphoprotein (P100) (P100) (Major antigenic
; DE structural protein).
; DE Ull OR P101F1.
; GN Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
; OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
; OC Betaherpesvirinae; Roseolovirus.
; OX NCBI_TaxID=10370;
; RN [1]
; RN RP
; RP SEQUENCE FROM N.A.
; RX MEDLINE=92260671; PubMed=1374813;
; RA Neipel F., Ellinger K., Fleckenstein B.;
; RA "Gene for the major antigenic structural protein (p100) of human
; RA herpesvirus 6.";
; RL J. Virol. 66:3918-3924(1992).
; RN [2]
; RN RP
; RP SEQUENCE FROM N.A.
; RX MEDLINE=94118404; PubMed=8289364;
; RA Nicholas J., Martin M.;
; RA "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
; RA genome of human herpesvirus 6 encoding human cytomegalovirus
; RA immediate-early gene homologs and transactivating functions.";
; RL J. Virol. 68:597-610(1994).
; RN [3]
; RN RP
; RP SEQUENCE FROM N.A.
; RX MEDLINE=95266321; PubMed=7747482;
; RA Campels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
; RA Martin M.E., Efsthaliou S., Craxton M., Macaulay H.A.;
; RA "The DNA sequence of human herpesvirus-6: structure, coding content,
; RA and genome evolution.";
; RL Virology 209:29-51(1995).
; CC -1- SIMILARITY: TO THE LARGE STRUCTURAL PHOSPHOPROTEINS OF HSV-7 AND
; CC HCMV UL32.
; CC
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; CC
; CC EMBL; M87287; AAA46012.1; -.
; CC EMBL; L25528; AAA16716.1; ALT_INIT.
; CC EMBL; X83413; CAA58438.1; -.
; CC Matrix protein; Phosphorylation.
; CC SEQUENCE 870 AA; 97071 MW; F25954DEA19BF824 CRC64;
;
; P100_HSV6U Length: 870 April 15, 2004 09:31 Type: P Check: 500
;
; P100_HSV6U
; MDLQSHPIPAWLDKVERLTDPLSLNLRDNDVDRHSHVTVNSCVVRGDDVDLKTLYNLVLWLMY
; HYLKSRPDYNAIWQDITKIQSVVNEVNSKLGKGIFFENFTNKEKPKSQPSDINAILRLGNFKMG
; SNVAIDTPVNTATDSSEIENNLOQAKNNLWTVYVINDPMDENGYLITISNKGLYGLKFLALQTSW
; SKLEKVASQITQNHLSLRDHNFNIVYSHRVQTLTGQORVESFLKITSYDIITKLSLESHSAS
; KAFMSSEIGPNLDFVPLRGDIHNSLTLPMSIDTKKSLDPAFLKNSRSLDSFLRQORQPKFLELD
; SYDNAGEKILLKAEATLGGENVKATTPASSSLMSGVSPSTNLDPLSSFTSLNLRDQKSHGNYK
; IGPQGLIDPNVKEFPNACLTNGVDLQDKTSGSPSGITDVVNGFANLNHONKSNVSPWNRNTAAN
; ADPLDPVRPEONGTFVLNNSDVAGSEAKHTYSTETGVSPRVFLIKDLRGKDPKQKQSDIPKS
; LTKERNDAIMHSREVTGSDGATETVGARNSPALRIKIQANDPFAGLNKQNDVDLVRGKGNKDLHS
; GNKKKMSGFNDKDNTRNGQPSRLMDGARNAGEQTIQAGLCQRVNNLSTNLTSLGKEGID
; ILONQORTELKATENKSGRESEANVEKILEVSNPQDMFNFLQNDLVQSPFPFLPADLSREJSDA
; SFKDADLDKLPNGEREIDDLAEKVKYGVGTETSLDKVGQDSFVPAQMKVETPEEKDIIIEQWLRIRQ
; DGETDENTVSGFVAESLDIEAKGESAIAS1

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TOIG of: pfda_metka check: 9337 from: 1 to: 157
ID PFDA_METKA STANDARD; PRT; 157 AA.
AC QSTUY7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prefoldin alpha subunit (GimC alpha subunit).
GN PFDA OR WK1614.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AV19 / DSM 6324 / JCM 9639;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
CC -!- FUNCTION: Molecular chaperone capable of stabilizing a range of
CC proteins. Seems to fulfil an ATP-independent, HSP70-like function
CC in archaeal de novo protein folding (By similarity).
CC -!- SUBUNIT: Heterohexamer of two alpha and four beta subunits (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the prefoldin alpha subunit family.
CC -----
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CC -----
DR EMBL; AE010451; AM02827.1; -
DR HAMAP; MF 00308; -; 1.
DR InterPro; IPR004127; DUF232.
DR Pfam; PF02996; Prefoldin; 1.
DR Chaperone; Complete proteome.
SQ SEQUENCE 157 AA; 17446 MW; B20BDA8CC978DPA1 CRC64;

PFDA METKA Length: 157 April 15, 2004 09:31 Type: P Check: 9337 ..
pfdametka
MAEKNKEQLQELQRIEINRLOGMNAIQAIDLEISSELNRYEETLKGVELEGDEEVLVPVGA
QSFVRACVTPTERVIGIGAVERTIDEALESIDDRQLEKARAEAAQQLQELQELQEKQKQEL
AQQLGQRIAAQSGGI
TOIG of: 033907 check: 3609 from: 1 to: 543
ID 033907; PRELIMINARY; PRT; 543 AA.
AC 033907;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Shewanella sp. SCRC-2738.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=53560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SCRC-2738;
RA MEDLINE=97419510; PubMed=9274025;
RA Takeyama H., Takeda D., Yazawa K., Yamada A., Matsunaga T.;
RT "Expression of the eicosapentaenoic acid synthesis gene cluster from
RT Shewanella sp. in a transgenic marine cyanobacterium, Synechococcus
RT sp."

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; RL Microbiology 143:0-0(0).
; DR EMBL; U73935; AAB81126.1; -.
; DR PIR; T30186; T30186.
; KW Hypothetical protein.
; SQ SEQUENCE 543 AA; 59378 MW; 7233F53635B794C7 CRC64;
;
; 033907 Length: 543 April 15, 2004 09:31 Type: P Check: 3609 ..
; 033907
; MPTATNEMLSWPWAVTESNISFDVQVMEHQLKDFSRACVYVNHADHGFGIAQTADIVTEQAANSTDLP
; VSAFTPALGTESLGDNPNRRVHGVIYIYAGAMANGISSEELVIALGQAGILCGFGAAGLIPSRVEAAI
; NRIQAALPGTFMFLIHSPEPALRGSEVLFKHKVRTVEASAFGLTPOIVYVYFAAGLSRDAQKVV
; VGNKVIKTSRTVEAKTFMFPAPAKMLQKLVDDGSITAEQMLAQVPMADDITAEADSGGHTDNRPLVT
; LLPTILAKKEEIQAKYQDTPTRVCGCGGVTGTPDAALATFNMGAAIYIVTGSINQACVEAGASDHTRKLIA
; TTMADVTMAPADMPFEMGVKLVVKGRTLPFRANKLYEITYRYSIEAIPLDEREKLEKQVFRSLDE
; INAGTVAHENERDKQIERRAGNPKRKVALIPRVGLGSSRWSNSGVGEMDQYQWAGPALGAFNQWAK
; GSILQNYQDRNAVDLAKHLMYGAAYINRINSLTAQGVKVPQAQLLRNKPQEMAI

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TOIG of: q97wg2 check: 6793 from: 1 to: 220

ID	Q97WG2	PRELIMINARY;	PRT;	220 AA.
AC	Q97WG2			
DT	01-OCT-2001 (TrEMBLrel. 18, Created)			
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Hypothetical protein SSO2259.			
GN	SSO2259.			
OS	Sulfolobus solfataricus.			
OC	Archaea; Erenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;			
OC	Sulfolobus.			
OX	NCBI_TaxID=2287;			
RN	[1]_SEQUENCE FROM N.A.			
RP	STRAIN=ATCC 35092 / DSM 1617 / P2;			
RC	MEDLINE=21332296; PubMed11427726;			
RX	She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,			
RA	Awayez M.J., Chan-Weiler C.C.-Y., Clausen I.G., Curtiss B.A.,			
RA	De Moors A., Erasuo G., Fletcher C., Gordon P.M.K.,			
RA	Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,			
RA	Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,			
RA	Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,			
RA	Garrett R.A., Ragan M.A., Sensen C.W. Van der Oost J.;			
RT	"The complete genome of the Erenarchaeon Sulfolobus solfataricus P2."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).			
DR	EMBL; AE006830; AAK42425.1; -;			
DR	PIR; B90396; B90396.			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 220 AA; 24900 MW; ECC55875E903DF2B CRC64;			
	Q97WG2 Length: 220 April 15, 2004 09:32 Type: P Check: 6793 ..			
	Q97wg2			
	MTNNGEYFALNLLKDEKLSNKLINLVINTDRGLDVGKILEDENTICKIGISLTSDDVLELLVND			
	YKTKTIFINEDNYIQLINLIDKRSKGLDPIGLLEDEESLKGKINALINLFTLNLIHWSEIF			
	NRDSISDITNFKYTLFVTSAGTALKNVTKTISWEIKYKLPDIFQRLGVAAASVLRKIGKLYPDK			
	GLAFVSEKLL			

[illegible]